

**RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
BIOSENSORS OF CHEMICAL SENSANTS**

5 **Cross Reference to Related Application**

This application is related to U.S. Provisional Serial No. 60/213,812, filed June 22, 2000, and U.S. Serial No. 09/804,291, filed March 13, 2001, which are incorporated by reference in their entirety.

10 **Background of the Invention**

Field of the Invention

The invention relates to the use of sensory G protein-coupled receptor complexes that recognize chemical sensants, particularly those involving olfactory and taste receptors; polypeptide fragments and mutants thereof; classes of such receptors; polynucleotides encoding such receptors, fragments and mutants thereof, and representatives of receptor classes; genetic vectors including such polynucleotides; and cells and non-human organisms engineered to express such receptor complexes, fragments and mutants of an olfactory or taste receptor, and representatives of receptor classes to simulate sensory perception of odorants and tastants. The invention also relates to the use of such products as a biosensor or component thereof to detect, to identify, to measure, or otherwise process the event of binding between the receptor and its cognate ligand (*i.e.*, chemical sensant). The invention has application, for example, in the design and formulation of odorant and tastant compositions.

25 Description of the Related Art

The olfactory and taste systems provide sensory information about the chemical environment. Olfactory receptors and taste receptors recognize, respectively, "odorants" and "tastants," collectively referred to as "sensants" or "sensory receptor ligands" herein. A "primary" sensant is an odorant or tastant ligand that substantially binds to sensory receptors with a ligand-binding site of a single amino acid sequence. Olfactory and taste receptors belong to the superfamily of seven-transmembrane guanyl nucleotide-binding proteins: such receptors are, however, also recognized as distinct families, or sub-genuses, of olfactory or taste

receptors (see Raming *Nature* 361:353, 1993). These receptors control diverse physiological functions such as media-ting signaling from an external chemical stimulus across the membrane containing the receptor into a cell, endocrine function, exocrine function, heart rate, lipolysis, and carbohydrate metabolism. Thus, the
5 dissection of these diverse functions into component signals is needed.

But the complexities of sensory perception of chemical sensants prevent easy translation of the olfaction and taste systems to a machine sensor. For example, U.S. Patent Nos. 5,675,070; 5,918,257; 5,928,609; and 6,085,576 disclose machine sensors that use various chemistries, but they do not take advantage of the specificity of
10 olfactory and taste receptors for their cognate ligands to produce a biosensor.

WO 00/15269 discloses methods and apparatus for odor reproduction. The total affinities of a specific odorant with a group of receptors was called the affinity fingerprint of the odorant. This odorant fingerprint was represented by a vector of affinity values. It was proposed to repro-duce an arbitrary odor by inputting its sensed
15 odorant fingerprint into a device, which has a palate of predetermined odorants and produces a composite odor using predetermined odorant finger-prints by minimizing the difference between vectors representing the sensed odorant fingerprint and the predetermined odorant fingerprints. This reference, however, does not teach or suggest the human olfactory receptors disclosed herein.

WO 00/70343 discloses biosensors and sense replication systems using G-protein coupled receptors (GPCR). It was proposed to mimic the response of the G-protein signal transduction system by detecting the affinity of a stimulus to a plurality of GPCR, codifying such information into electronic signals, and reproducing the stimulus by converting the codified information into a combination of stimulant
20 entities. But this reference also does not teach or suggest the human olfactory receptors disclosed herein.

WO 01/27158 discloses olfactory receptors and their use to determine the correspondence between individual odorant receptors and particular odors. It was proposed that the interactions between an odor and olfactory receptors can be used to
30 represent the odor and to re-create it. This reference, however, does not teach or suggest the human olfactory receptors disclosed herein.

Dissecting the function of sensory receptors by binding sensory receptors of a clone of cells expressing a single sensory receptor gene, fragmentation of sensory

receptors to provide ligand-binding or signal-transducing domains thereof, and construction of fusion sensory recep-tor proteins will separate the diverse physiological functions associated with sensory perception at the level of ligand-receptor binding. Furthermore, novel “primary sensants” that are identified and isolated by the methods described herein may be used to further define the function of the cognate sensory receptor by uniquely enhancing or, in the alternative, blocking stimulation of sensory receptors with a single ligand-binding domain.

The present invention addresses the need for better understanding of these ligand-receptor interactions by using a large set of identified sensory receptors. Even if the receptor set used is incomplete (*i.e.*, a partial set of all sensory receptors encoded in the genome), a large number of sensants will be detected. Moreover, redundancy in the chemical structures recognized by the sensory receptors or combinatorial processing of signals from different sensory receptors would allow broad coverage of chemically diverse sensants (*e.g.*, by selection of a representative class of sensory receptors). Also provided are, *inter alia*, methods for utilizing such sensory receptors and biosensors to simulate sensory perception. To analyze ligand-receptor interactions and their effects on cell signaling and the processing of those signals in sensory perception, specific sensants and their cognate receptor complexes are detected, identified, and measured under binding conditions. Fragrances and flavorings can be detected, identified, measured, and/or custom designed by the methods herein described. In addition, drugs that incorporate artificial odors and/or tastes can be formulated.

Summary of the Invention

Large gene families encoding mammalian olfactory G-protein-coupled receptors (OLFR) and mammalian taste G-protein-coupled receptors (TASR) are known in the prior art or are disclosed herein. An object of the invention to provide fragments and variants of such OLFRs and TASRs which retain odorant- or tastant-binding activity, respectively. The large number of sensory receptors that are made available herein and now amendable to manipulation raises the confidence that a substantially complete, or at least functional, repertoire of sensory receptors is provided.

It is an object of the invention to provide nucleic acid sequences or molecules that encode such sensory receptors, or fragments or variants thereof. Another object is to provide expression vectors which include nucleic acid sequences that encode such sensory receptors, or fragments or variants thereof. It is yet another object of the invention to provide human or non-human cells which functionally express at least one of such sensory receptors, or fragments or variants thereof. Still another object is to provide sensory receptor fusion proteins or other polypeptides which include at least a fragment of at least one of such sensory receptors. In particular, fusions with reporter molecules or other heterologous amino acid sequences may maintain the original ligand-properties while changing the signaling properties to allow easier detection of sensant binding to the receptor (*e.g.*, change in fluorescent signal). Moreover, chimeric proteins or other polypeptides with altered ligand-binding and/or signaling properties can be made from two or more different sensory receptors by mixing domains.

The invention provides methods for representing the sensory perception of one or more chemicals (*e.g.*, a primary sensant or mixture thereof) and/or for predicting the sensory perception of one or more chemicals in a mammal (*e.g.*, human) using the aforementioned products. Given a known member of a ligand-receptor binding pair, one or both members of the pair (*i.e.*, ligand, receptor, or both) may be detected, identified, and/or measured under binding conditions.

Novel molecules or combinations of molecules which elicit a desired and predetermined sensory perception in a mammal (*e.g.*, human) can be generated by determining a value of sensory perception in a mammal for a known molecule or combination thereof; determining a value of sensory perception in a mammal for one or more unknown molecules or combinations thereof; comparing the value of sensory perception in a mammal for one or more unknown compositions to the value of sensory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined sensory perception in a mammal; and mixing two or more unknown molecules or combinations thereof to form a molecule or combination thereof that elicits a predetermined sensory perception in a mammal. The combining step yields a single molecule or a combination thereof that elicits a predetermined sensory perception in a mammal. In particular, primary odorants that uniquely bind to olfactory receptors with a single

ligand-binding domain may be such novel molecules. Variants thereof may be used (1) to enhance stimulation of a limited response by olfactory receptors with a single ligand-binding domain or (2) to block stimulation of olfactory receptors with a single ligand-binding domain to reduce or inhibit olfactory perception. An alternative method for identifying primary odorants is to identify the mutated receptors in genetic anosmias because that odorant would be expected to be recognized by only one or a few olfactory receptors affected by the mutation.

Detailed Description of the Invention

10 Perception of Chemical Sensants

U.S. Patent No. 5,691,188 describes how upon binding of ligand to receptor, the receptor presumably undergoes a conformational change leading to activation of the G protein. The G proteins are comprised of three subunits: a guanyl nucleotide binding α subunit, a β subunit, and a γ subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the α subunit. When GDP is bound, the G protein exists as a heterotrimer: the $G\alpha\beta\gamma$ complex. When GTP is bound, the α subunit dissociates from the heterotrimer, leaving a $G\beta\gamma$ complex. When a $G\alpha\beta\gamma$ complex operatively associates with an activated G protein coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of disso-ciation of the bound $G\alpha$ subunit from the $G\alpha\beta\gamma$ complex increases. The free $G\alpha$ subunit and $G\beta\gamma$ complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell. A high-resolution X-ray crystal structure is available for rhodopsin, a guanyl nucleotide binding protein, has been solved (Palczewski *et al.*, *Science* 289:739, 2000). Using this structure, the portions of the amino acid sequence of sensant receptors that are responsible for ligand binding can be identified.

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Sensory Perception - Olfaction

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel *Sci. Amer.* 273:154, 1995). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer *Semin. Cell Biol.* 5:25, 1994). The human genome contains thousands of genes that encode a diverse repertoire of olfactory receptors (Rouquier *Nat. Genet.* 18:243, 1998; Trask *Hum. Mol. Genet.* 7:2007, 1998). An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that sensory receptors belong to a multigene family with over a thousand members, and the odorant receptors number at least 500 to 1,000. Moreover, each sensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses.

Sensory Perception - Taste

Mammals are believed to have five basic taste modalities: sweet, bitter, sour, salty, and umami (the taste of monosodium glutamate). *See, e.g., Kawamura et al., Introduction to Umami: A Basic Taste* (1987); Kinnamon *et al., Ann. Rev. Physiol.*, 54:715, 1992; Lindemann, *Physiol. Rev.*, 76:718, 1996; Stewart *et al., Am. J. Physiol.*, 272:1, 1997. Numerous physiological studies in animals have shown that taste receptor cells may selectively respond to different chemical stimuli. *See, e.g., Akabas et al., Science*, 242:1047, 1988; Gilbertson *et al., J. Gen. Physiol.*, 100:803, 1992; Bernhardt *et al., J. Physiol.*, 490:325, 1996; Cummings *et al., J. Neurophysiol.*, 75:1256, 1996.

In mammals, taste receptor cells are assembled into taste buds that are distributed into different papillae in the tongue epithelium. Circumvallate papillae, found at the very back of the tongue, contain hundreds, *e.g., mice*, to thousands, *e.g., human*, of taste buds. By contrast, foliate papillae, localized to the posterior lateral edge of the tongue, only contain dozens to hundreds of taste buds. Moreover, fungiform papillae contain only a single or a few taste buds, and are at the front of the tongue.

Each taste bud, depending on the species, contains 50-150 cells, including precursor cells, support cells, and taste receptor cells. *See, e.g., Lindemann, Physiol. Rev.*, 76:718, 1996. Receptor cells are innervated at their base by afferent nerve endings that transmit information to the taste centers of the cortex through synapses in the brain stem and thalamus. Elucidating the mechanisms of taste cell signaling and information processing is critical for understanding the function, regulation, and perception of the sense of taste.

Exemplary bitter substances are of 6-n-propylthiouracil (PROP), sucrose octaacetate (soa), raffinose undecaacetate (rua), cycloheximide (cyx), denatonium, copper glycinate (GI), and quinine (qui), which bind one or more T2R taste receptors.

Structure of Receptors for Chemical Sensants

Complete or partial sequences of numerous human and other eukaryotic sensory receptors are currently known. *See, e.g., Pilpel et al., Protein Sci.*, 8:969, 1999; Mombaerts, *Annu. Rev. Neurosci.*, 22:487, 1999. *See also*, EP0867508A2, US 5874243, WO 92/17585, WO 95/18140, WO 97/17444, WO 99/67282.

Genes encoding two hundred fifty-six (256) distinct, novel human olfactory receptors have been identified in genome sequence databases. All of the receptor genes have been initially detected by a computer DNA sequence analysis in the corresponding partially sequenced human BAC genomic clones (unfinished High Throughput Genomic Sequence database accession numbers AB045359, AP002532, AP002533, AL365440, AC073487, AL359636, AL359,955, AP002535, AB045365, AL359218, AC002555, AB045361, AL359512, AC023255, AL358773, AL357767, AL358874, AC068380, AC025283, AP002407, AC018700, AC022289, AC006313, AC002556, AC011571, AL121944, AC007194, AP001112, AC021660, AP000723, AC016856, AC018700, AP000818, AC00596, AP000916, AC011517, AP001112, AP000916, AC021427, AC021427, AC020884, AC019108, AL135841, AL133410, AF186996, AL138834, AC009237, AC025249, AC010930, AC009758, AC009642, AC009758, AC025249, AF101706, AC009642, AC025249, AC021660, AC011647, AC011711, AC09642, AC020597, AC011711, AC019088, AC022882, AC011571, AL121944, AP000435, AC012616, AC010332, AC010766, AP000743, AC021809, AC011879, AC021304, AC023226, AL160314, AC021304, AC020380, AC011904, AC004977, AC021304, AP000868, AP000825, AC023080, AC022207, AC121986,

AC010814, AC018700, AC021304, AC008620, AC011537, AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, 5 AP001803, AP001804, AL353767, AP001884, AC026083, AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, 10 AP002826, AL359636, AL391534, AC055731, AC076959, AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes. Similarly, genes encoding five and thirty-six (36) distinct, novel human T1R and T2R taste receptors, respectively, have been identified in genome 15 sequence databases.

Alternatively, nucleic acids encoding the sensory receptors and other related polypeptides can be isolated from a variety of sources, genetically engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 00/35374, which is herein incorporated by reference in its entirety.

20 These nucleic acids provide probes for the identification of cells expressing sensory receptors, as the nucleic acids are specifically expressed in such cells. They can also serve as tools for the generation of sensory topographical maps that elucidate the relationship between cells expressing sensory receptors and sensory neurons leading to particular regions of the brain. Furthermore, the nucleic acids and the 25 polypeptides they encode can be used as probes to elucidate olfactant- or tastant-induced behaviors.

Nucleic acid molecules encoding a sensory receptor comprising a nucleic acid sequence that is at least 75%, 85%, 90%, 95%, or 99% identical to a nucleic acid sequence selected from those known in the prior art or disclosed herein are considered 30 variants. Other nucleic acid molecules comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence at least 75%, 85%, 90%, 95%, or 99% identical to an amino acid sequence selected from those known in the prior art or disclosed herein are also considered variants. Further variants contain amino acid

sequence differences in at most ten, five, four, three, two, or one amino acid residue(s).

Exemplary nucleic acid sequences may be selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID

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 25 NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504,
 SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510; and SEQ ID NO: 512.

Nucleic acid molecule comprising a nucleic acid sequence that encodes a
 fragment of a polypeptide having an amino acid sequence selected from those known
 in the prior art or disclosed herein; wherein the fragment is at least ten, 20, 30, 50, 70,
 30 100, or 150 amino acid residues in length, are useful as probes, primers, and to
 construct hybrids or chimerae.

Polypeptides comprising an amino acid sequence that is at least 90%, 95%,
 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from those

known in the prior art or disclosed herein are considered variants. Further variants contain amino acid sequence differences in at most ten, five, four, three, two, or one amino acid residue(s). Other polypeptides comprising a fragment of a polypeptide having an amino acid sequence selected from those known in the prior art or disclosed herein; wherein the fragment is at least 40, 60, 80, 100, 150, 200, or 250 amino acid residues in length, are useful as specific binders of sensants, competitive binders, antigens, and to construct hybrids or chimerae.

Exemplary amino acid sequences may be selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235,

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25 SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID
NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469,
SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID
NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487,
SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID

30 NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505,
SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

Also provided are methods of screening for modulators, *e.g.*, activators, inhibitors, stimu-lators, enhancers, agonists, and antagonists, of the sensory receptors,

or fragments or variants thereof. Such modulators of signal transduction are useful for pharmacological or genetic modulation of signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of sensory cell activity. These modulator compounds can then be used in the pharmaceutical, food, and cosmetic industries to customize odorants or tastants.

Thus, the invention provides assays for sensory modulation, where the sensory receptors, or fragments or variants thereof, act as direct or indirect reporter molecules for the effect of modulators on signal transduction. Sensory receptors, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo*, and *ex vivo*. In one embodiment, sensory receptors, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g.*, Mistili *et al.*, *Nature Biotech.*, 15:961, 1997). In another embodiment, the sensory receptors, or fragments or variants thereof, can be expressed in host cells, and modulation of signal transduction via sensory receptor activity can be assayed by measuring changes in Ca^{2+} levels.

Methods of assaying for modulators of signal transduction include *in vitro* ligand binding assays using the sensory receptors, or fragments or variants thereof. More particularly, such assays can use the sensory receptors; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G-protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular Ca^{2+} levels; and neurotransmitter release.

The invention also provides for methods of detecting sensory receptor nucleic acid and protein expression, allowing for the investigation of taste transduction regulation and specific identification of sensory receptor cells. The sensory receptors, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying a sensory receptor cells. Sensory receptor cells can be identified using techniques such as reverse transcription and amplification

of mRNA, isolation of total RNA or poly A⁺ RNA, Northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, Western blots, and the like.

A. Identification and Characterization of Sensory Receptors

5 The amino acid sequences of the sensory receptors and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

10 For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as
15 described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

20 A “comparison window,” as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment
25 of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443, 1970, by the search for similarity method of Pearson & Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and
30 TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nucl. Acids Res.* 25:3389, 1977 and Altschul *et al.*, *J Mol. Biol.* 215:403, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nucl. Acids Res.* 25:3389, 1977 and Altschul *et al.*, *J. Mol. Biol.* 215:403, 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad Sci. USA* 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-called "tree" or "dendrogram" showing the clustering relationships used to create the alignment (*see, e.g.*, Figure 2). PILEUP uses a simplification of the progressive

alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351, 1987. The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151, 1989. The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the

5 pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by

10 designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can

15 be obtained from the GCG sequence analysis software package, *e.g.*, version 7. 0 (Devereaux *et al.*, *Nucl. Acids Res.* 12:387, 1984) encoded by the genes were derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian

20 olfactory receptor family, each of the olfactory receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative sensory receptor proteins generally having lengths of about 300 to

25 about 400 amino acid residues that contain seven transmembrane domains, as predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the 256 sensory receptors identified herein has a characteristic sequence signature of an olfactory

30 receptor. In particular, all 256 sequences contain very close matches to the following consensus amino acid motifs (Mombaerts, 1999; Pilpel, 1999): LHTPMY in intracellular loop 1, MAYDRYVAIC at the end of transmembrane domain 3 and the beginning of intracellular loop 2 , SY at the end of transmembrane domain 5,

FSTCSSH in the beginning of transmembrane domain 6, and PMLNPF in transmembrane domain 7. Combination of all the above mentioned structural features of the 256 genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

5 As noted above, complete or partial sequences of numerous human and other eukaryotic sensory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human sensory receptors, which suggests their different specificity in sensant recognition. Therefore, these novel sensory receptors and their genes can be used, alone or in combination
10 with known sensory receptors, in developing detection systems and assays for chemically distinct types of sensants not recognized by the known sensory receptors, as well as for diagnostic and research purposes.

B. Definitions

The terms "purified," "substantially purified," and "isolated" as used herein
15 refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the
20 compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or
25 concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or
30 proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

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The terms "amplifying" and "amplification" refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.*, specific degenerate oligonucleotide primer pairs) for amplifying (*e.g.*, by polymerase chain reaction, PCR) naturally expressed (*e.g.*, genomic or mRNA) or recombinant (*e.g.*, cDNA) nucleic acids of the invention (*e.g.*, sensant-binding sequences of the invention) *in vivo* or *in vitro*.

The term "7- transmembrane receptor" means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma membrane seven times (thus, the seven domains are called "transmembrane" or "TM" domains TM I to TM VII). The families of olfactory and taste receptors each belong to this super-family. Seven-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

The term "expression vector" refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, *i.e.*, drive only transient expression in a cell. The term includes recombinant expression "cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

The term "library" means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated sensory, particularly olfactory or taste, receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of vectors that incorporate the amplified sensant-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding a sensory receptor.

The term "nucleic acid" or "nucleic acid sequence" refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded form. The term encompasses nucleic acids, *i.e.*, oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like

structures with synthetic backbones, *see e.g., Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Anti-sense Strategies*, Annals of the N.Y. Academy of Sciences, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan (1993) *J. Med. Chem.* 36:1923-1937; *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata (1997) *Toxicol. Appl. Pharmacol.* 144:189-197; Strauss-Soukup (1997) *Biochemistry* 36:8692-8698; Samstag (1996) *Antisense Nucleic Acid Drug Dev* 6:153-156.

The term sensory receptor “ligand-binding region” refers to sequences derived from a sensory receptor that substantially incorporates transmembrane domains II to VII (TM II to VII). The domain may be capable of binding a sensant.

The terms “conservative variant” or “analog” or “mimetic” refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the poly-peptide’s (the conservative variant’s) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, etc.) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity. Conservative substitution tables providing function-ally similar amino acids are well known in the art.

For example, one exemplary guideline to select conservative substitutions includes (original residue followed by exemplary substitution): Ala/Gly or Ser; Arg/Lys; Asn/Gln or His; Asp/Glu; Cys/Ser; Gln/Asn; Gly/Asp; Gly/Ala or Pro; His/Asn or Gln; Ile/Leu or Val; Leu/Ile or val; Lys/Arg or Gln or Glu; Met/Leu or Tyr or Ile; Phe/Met or Leu or Tyr; Ser/Thr; Thr/Ser; Trp/Tyr; Tyr/Trp or Phe; Val/Ile or Leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g., Creighton, Proteins*, W.H. Freeman, 1984; Schultz & Schimer, *Principles of Protein Structure*, Springer-Verlag, 1979). One of skill in the art will appreciate that the above-identified substitutions are not the only possible

conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered “conservatively modified variations.”

The terms “mimetic” and “peptidomimetic” refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains or sensant-binding domains or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or, is a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic’s structure and/or activity. As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond (“peptide bond”) linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, *i.e.*, to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N’-dicyclohexylcarbodiimide (DCC) or N,N’-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond (“peptide bond”) linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH₂- for -C(=O)-NH-), aminomethylene (CH₂-NH), ethylene, olefin (CH=CH), ether (CH₂-O), thioether (CH₂-S), tetrazole (CN₄), thiazole, retroamide, thioamide, or ester (see, *e.g.*, Spatola (1983) in *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, Vol. 7, pp 267-357, “Peptide Backbone Modifications,”

Marcell Dekker, NY). A polypeptide can also be characterized as a mimetic by containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (e.g., "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, e.g., inducible or constitutive expression of a fusion protein comprising a translocation domain of the invention and a nucleic acid sequence amplified using a primer of the invention.

The term "transmembrane domain" means a polypeptide domain that can completely span the plasma membrane. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below.

C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the sensory receptors, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand binding regions and libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (e.g., promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can
5 be used, including, in addition to mammalian cells, *e.g.*, bacterial, yeast, insect or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, *e.g.*, Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983);
10 Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the
15 strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature.
20 *See, e.g.*, Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I, Theory and Nucleic Acid Preparation*, Tijssen, ed. Elsevier, N.Y. (1993).

25 Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, *e.g.*, analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion
30 chromatography, various immunological methods, *e.g.*, fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassay (RIA), enzyme-linked immunosorbent assay (ELISA), immunofluorescent assay, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (*e.g.*, SDS-PAGE),

RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (*PCR Protocols, a Guide to Methods and Applications*, ed. Innis. Academic Press, NY, 1990 and *PCR Strategies*, ed. Innis, Academic Press, NY, 1995), ligase chain reaction (LCR) (see, e.g., Wu, *Genomics* 4:560, 1989; Landegren, *Science* 241:1077, 1988; Barringer, *Gene* 89:117, 1990); transcription amplification (see, e.g., Kwok, *Proc. Natl. Acad. Sci. USA* 86:1173, 1989); and, self-sustained sequence replication (see, e.g., Guatelli, *Proc. Natl. Acad. Sci. USA* 87:1874, 1990); Q Beta replicase amplification (see, e.g., Smith, *J. Clin. Microbiol.* 35:1477, 1997); automated Q-beta replicase amplification assay (see, e.g., Burg, *Mol. Cell. Probes* 10:257, 1996) and other RNA polymerase mediated techniques (e.g., NASBA, Cingone, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307, 1987; Sambrook; Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563, 1995.

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, e.g., U.S. Patent No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that, when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the sensant-binding region-coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted sensant-binding domain comprises substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I

and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify sensant-binding regions of olfactory receptor proteins. These domain regions may vary for different sensants, and more particularly odorants; thus, what may be a minimal binding region for one sensant, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane sensory receptor.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL. Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII.

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3'). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify a transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL, encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CA-NGT-3'. Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (*see, e.g.,* Rose, *Nucl. Acids Res.* 26:1628, 1998; Singh, *Biotechniques* 24:318, 1998).

Means to synthesize oligonucleotide primer pairs are well known in the art. "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g.,* Hoops, *Nucleic Acids Res.* 25:4866, 1997. Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g.,* Morales, *Nat. Struct. Biol.* 5:950, 1998). For example, two degenerate bases can be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g.,* Hill, *Proc. Natl. Acad. Sci. USA* 95:4258, 1998). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine, 3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, *see* above). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3'.
5
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' and
5'-GGGGCTGCAGACACC(AC/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3'.
10
- (c) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)GG-3' and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3'.
15

Nucleic acids that encode ligand-binding regions of olfactory receptors are generated by amplification (*e.g.*, PCR) of appropriate nucleic acid sequences using degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, *e.g.*, olfactory neurons or olfactory epithelium.
20

Isolation from olfactory receptor-expressing cells is well known in the art (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (*see, e.g.*, Buiakova, *Proc. Natl. Acad. Sci. USA* 93:9858, 1996). Shirley, *Eur. J. Biochem.* 32:485, 1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211, 1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, *e.g.*,
35

antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260, 1999), describes differentiated olfactory receptor-expressing cells in culture that respond to odorants, as measured by an influx of calcium.

5 Hybrid protein-coding sequences comprising nucleic acids sensory receptors fused to the translocation sequences described herein may be constructed. Also provided are hybrid receptors comprising the translocation motifs and ligand-binding domains of sensory receptors. These nucleic acid sequences can be operably linked to transcriptional or translational control elements, *e.g.*, transcription and translation
10 initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can
15 also be used to express the fusion polypeptide receptor, including, *e.g.*, a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227, 1998). Receptor genes are normally expressed in a small subset of
20 neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

 Fusion proteins, either having C-terminal or, more preferably, N-terminal
25 translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized
30 metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g., Ottavi, Biochimie* 80:289, 1998), subtilisin protease recognition motif (*see, e.g., Polyak, Protein Eng.* 10:615, 1997); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a nucleic acid sequence encoding a polypeptide linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g., Williams, Biochemistry* 34:1787, 1995), and an amino terminal translocation domain. The histidine residues facilitate detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature, *see, e.g., Kroll, DNA Cell. Biol.* 12:441, 1993).

Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent literature. *See, e.g., Roberts, Nature* 328:731, 1987; Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10, 1995; Sambrook; Tijssen; Ausubel. Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (*e.g., episomal expression systems*). Selection markers can be incorporated into expression cassettes and vectors to confer a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (*e.g., chloramphenicol, kanamycin, G418, bleomycin, hygromycin*) or herbicide resistance (*e.g., chlorosulfuron or Basta*) to permit selection of those cells transformed with the desired DNA sequences (*see, e.g., Blondelet-Rouault, Gene* 190:315, 1997; Aubrecht, *J. Pharmacol. Exp. Ther.* 281:992, 1997). Because

selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

5 A chimeric nucleic acid sequence may encode a sensant-binding domain within any 7-transmembrane polypeptide. Seven-transmembrane receptors belong to a superfamily of trans-membrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-trans-membrane receptor polypeptides have similar primary sequences and secondary and tertiary structures, structural domains
10 (*e.g.*, TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that characterize profiles of the hydrophobicity and variability of analyzed sequences. To
15 predict TM domains and their boundaries and topology, a “neural network algorithm” by “PHD server” can be used, as done by Pilpel, *Protein Science* 8:969, 1999; Rost, *Protein Sci.* 4:521, 1995. Periodicity detection enhancement and alpha helical periodicity index can be done as by, *e.g.*, Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.*, Peitsch,
20 *Receptors Channels* 4:161, 1996; Cronet, *Protein Eng.* 6:59, (1993) (homology and “discover modeling”); <http://bioinfo.weizmann.ac.il/>.

The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, *e.g.*, TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (*e.g.*, PCR) from mRNA of or cDNA derived
25 from, *e.g.*, olfactory receptor-expressing neurons or genomic DNA.

Libraries of sensory receptor ligand-binding TM domain sequences can include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the
30 seven domains can be identified by various analyses well known in the art, including, *e.g.*, homology modeling, Fourier analysis and helical periodicity (*see, e.g.*, Pilpel *supra*), as described above. Using this information sequences flanking the seven

domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of,
5 for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the sensory receptors described herein, coupled to additional amino acids representing all or part of another
10 G protein receptor, preferably a member of the 7-transmembrane superfamily. These chimerae can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the 7-transmembrane protein described herein, and the
15 remaining portion or portions come from another G protein-coupled receptor.

Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled in the art can readily be used to create such chimeric receptors. The use of such
20 chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand binding domain, an extracellular
25 domain, a transmembrane domain (e.g., one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous CGPCR
30 extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, e.g., green fluorescent protein, β -gal, glutamate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to a sensory receptor disclosed herein can be isolated using the nucleic acid probes described above. Alternatively, expression libraries can be used to isolate sensory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against a sensory receptor-derived polypeptide, which also recognize and selectively bind to the sensory receptor homolog.

Also within the scope of the invention are host cells for expressing the sensory receptors, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the sensory receptors, fragments, or variants thereof, the nucleic acid sequence of interest is subcloned into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable prokaryotic and eukaryotic expression systems are well known in the art and described, e.g., in Sambrook *et al.*

Any of the well known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasmid vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.,* Sambrook *et al.*). It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.,* WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

D. Immunological Detection of Sensory Receptor Polypeptides

In addition to the detection of sensory receptor genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect

sensory receptors, *e.g.*, to identify olfactory receptor cells, and variants of sensory receptor family members. Immunoassays can be used to qualitatively or quantitatively analyze the sensory receptors. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

5 1. Antibodies to sensory receptor family members

Methods of producing polyclonal and monoclonal antibodies that react specifically with a sensory receptor family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology*, 1991; Goding, *Monoclonal Antibodies: Principles and Practice*, 2d ed., 1986; Harlow & Lane, *supra*; and Kohler & Milstein, *Nature*, 256:495, 1975). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by immunizing rabbits or mice (*see, e.g.*, Huse *et al.*, *Science*, 246:1275, 1989; Ward *et al.*, *Nature*, 341:544, 1989).

15 A number of sensory receptor-comprising immunogens may be used to produce antibody specifically reactive with a sensory receptor family member. For example, a recombinant sensory receptor protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the conserved motifs that are used to identify members of the sensory receptor family.

20 Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Naturally occurring

25 protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in

30 the art. Mice, hamsters, rats, guinea pigs, rabbits, goats, or chickens is immunized with the protein using an adjuvant (*e.g.*, Freund's adjuvant) and a standard immunization protocol with periodic boosts. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of

reactivity to the sensory receptor. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (see Harlow & Lane, *supra*).

5 Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen are immortalized, commonly by fusion with a myeloma cell (see Kohler & Milstein, *Eur. J. Immunol.*, 6:511, 1976). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, retroviruses, or other
10 methods well known in the art. Colonies arising from single clones of immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a vertebrate host. Alternatively, one may isolate DNA sequences which encode a
15 monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275, 1989.

 Monoclonal antibodies or polyclonal sera are collected and titered against antigen in an immunoassay, for example, a solid phase immunoassay with the antigen
20 immobilized on a solid support. Typically, polyclonal antisera with a titer of 10^4 or greater are selected and tested for their cross reactivity against non-sensory receptor proteins, or even other sensory receptor family members or other related proteins from other organisms, using a competitive binding immuno-assay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a K_d of at least about 0.1
25 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

 Once sensory receptor family member specific antibodies are available, individual sensory receptor proteins can be detected by a variety of immunoassay methods. For a review of immuno-nological and immunoassay procedures, see *Basic and Clinical Immunology* (Stites & Terr eds., 7th ed., 1991). Moreover, the
30 immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*.

2. Immunological binding assays

Sensory receptor proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (see, e.g., U.S. Patent Nos. 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general
5 immunoassays, see also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993); *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed., 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case a sensory receptor family member or an antigenic subsequence thereof). The antibody (e.g., anti-sensory
10 receptor) may be produced by any of a number of means well known to those of skill in the art and as described above.

Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent
15 may be a labeled sensory receptor polypeptide or a labeled anti-sensory receptor antibody. Alternatively, the labeling agent may be a third moiety, such a secondary antibody, that specifically binds to the antibody/sensory receptor complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding
20 immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (see, e.g., Kronval *et al.*, *J. Immunol.*, 111:1401, 1973; Akerstrom *et al.*, *J. Immunol.*, 135:2589, 1985). The labeling agent can be modified with a detectable moiety, such as biotin, to which
25 another molecule can specifically bind, such as streptavidin. A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the
30 incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

a. Non-competitive assay formats

Immunoassays for detecting a sensory receptor protein in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays directly measure the amount of antigen. In one preferred “sandwich” assay, for example, the anti-sensory receptor antibodies are bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the sensory receptor protein present in the test sample. The sensory receptor protein thus immobilized is then bound by a labeling agent, such as a second anti-sensory receptor antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g.*, streptavidin, to provide a detectable moiety.

b. Competitive assay formats

In competitive assays, the amount of sensory receptor protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) sensory receptor protein displaced (competed away) from an anti-sensory receptor antibody by the unknown sensory receptor protein present in a sample. In one competitive assay, a known amount of sensory receptor protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the sensory receptor. The amount of exogenous sensory receptor protein bound to the antibody is inversely proportional to the concentration of sensory receptor protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of sensory receptor protein bound to the antibody may be determined either by measuring the amount of sensory receptor protein present in a sensory receptor/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of sensory receptor protein may be detected by providing a labeled sensory receptor molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known sensory receptor protein is immobilized on a solid substrate. A known amount of anti-sensory receptor antibody is added to the sample, and the sample is then contacted with the immobilized sensory receptor. The amount of anti-sensory receptor antibody bound to the known immobilized sensory receptor protein is

inversely proportional to the amount of sensory receptor protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, sensory receptor proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the sensory receptor polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percentage cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the sensory receptor family can be used in cross-reactivity determinations.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a sensory receptor family member, to the immunogen protein (*i.e.*, sensory receptor protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to

specifically bind to the polyclonal antibodies generated to a sensory receptor immunogen.

Antibodies raised against sensory receptor conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the sensory receptor family, but not to GPCRs from other families. Polyclonal antibodies that specifically bind to a particular member of the sensory receptor family, can be made by subtracting out cross-reactive antibodies using other sensory receptor family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human T2R01 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OLFR1 or mouse OLFR1.

d. Other assay formats

Western blot (immunoblot) analysis is used to detect and quantify the presence of sensory receptor protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind the sensory receptor protein. The anti-sensory receptor polypeptide antibodies specifically bind to the sensory receptor polypeptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-sensory receptor antibodies.

Other assay formats include liposome immunoassays (LIA) using liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see Monroe et al., Amer. Clin. Prod. Rev.*, 5:34, 1986).

e. Reduction of non-specific binding

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein

compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

f. Labels

5 The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immuno-assays and, in general, most any label useful in such methods can be applied to the present invention. Thus, a label is any composition
10 detectable by spectroscopic, photochemical, bio-chemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (e.g., DYNABEADS™, fluorescent dyes (e.g., fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (e.g., ³H, ¹²⁵I, ³⁵S, ¹⁴C, or ³²P), enzymes (e.g., horseradish peroxidase, alkaline phosphatase and others
15 commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (e.g., polystyrene, polypropylene, latex, etc.).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease
20 of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (e.g., biotin) is covalently bound to the molecule. The ligand then binds to another molecules (e.g., streptavidin) molecule, which is either inherently
25 detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a sensory receptor protein, or secondary antibodies that recognize anti-sensory receptor.

The molecules can also be conjugated directly to signal generating
30 compounds, e.g., by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone,

etc. Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, e.g., luminol. For a review of various labeling or signal producing systems that may be used, see U.S. Patent No. 4,391,904.

Methods for detecting labels are well known. Thus, for example, where the label is a radioactive label, it may be detected using a scintillation counter or with photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluoro-chrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, with photographic film, or using electronic detectors such as charge coupled devices (CCDs) or photomultipliers. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally, simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

E. Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian sensory, and more particularly, olfactory receptor of the invention, both *in vitro* and *in vivo* are described below, as are methods and compositions for determining whether a test compound is neurotoxic to an olfactory neuron expressing an olfactory transmembrane receptor polypeptide. Any aspect of cell physiology can be monitored to assess the effect of sensant-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical

stimuli into electrical signals. An activated or inhibited G-protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G-protein, phospholipase C by Gq and other cognate G-proteins, and modulation of diverse channels by Gi and other G-proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The sensory receptor protein of the assay will typically be selected from a natural poly-peptide or conservatively modified variant thereof. Generally, the amino acid sequence identity will be at least 75%, 85%, 90%, 95%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of a sensory receptor protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand binding domain, subunit association domain, active site, and the like. Either the sensory receptor protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein.

Modulators of sensory receptor activity can be tested using sensory receptor polypeptides as described above, either recombinant or naturally occurring. Protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

1. *In vitro* binding assays

Sensory perception can also be examined *in vitro* with soluble or solid state reactions, using a full-length sensory receptor-GPCR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a sensory receptor covalently linked to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of a sensory receptor. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises all or part of a sensory receptor polypeptide, as well an additional sequence that facilitates the localization of the

sensory receptor to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein.

Ligand binding to a sensory receptor protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid
5 monolayer, or in vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties. Sensory receptors with large (*e.g.*, approximately 600 amino acid residues) extracellular N-terminal segments. These N-terminal segments are thought to form ligand-binding
10 domains, and are therefore useful in biochemical assays to identify sensory receptor agonists and antagonists. Similar assays have been used with other GPCRs, such as the metabo-tropic glutamate receptors (*e.g.*, Han & Hampson, *J. Biol. Chem.* 274:10008, 1999). These assays might involve displacing a radioactively or fluorescently labeled ligand, and measuring changes in intrinsic fluorescence or
15 changes in proteolytic susceptibility, *etc.*

Receptor-G-protein interactions can also be examined. For example, binding of the G-protein to the receptor or its release from the receptor can be examined. For example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be
20 detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits
25 serves as a criterion of activation.

An activated or inhibited G-protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G-protein, phospholipase C by Gq and other cognate G
30 proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization (“FP”) based assays may be used to detect and monitor sensant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation, or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the sensory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nano-seconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the sensory receptors of the invention, fluorescence-labeled sensants or auto-fluorescent sensants may be used. Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

Where \parallel is the intensity of the emission light parallel to the excitation light plane and Int_{\perp} is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For

example, the Beacon® and Beacon 2000™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley *J. Anal. Toxicol.* 5, 236, 1981 which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity (η), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$\text{Rotational Relaxation Time} = \frac{3\eta V}{RT}$$

The rotational relaxation time is small (≈ 1 nanosecond) for small molecules (*e.g.*, fluorescein) and large (≈ 100 nanoseconds) for large molecules (*e.g.*, immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

3. Soluble and solid state high throughput assays

In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, *etc.*; a domain that is covalently linked to a heterologous protein to create a chimeric molecule; a sensory receptor protein; or a cell or tissue expressing a sensory receptor protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based *in vitro* assays in a high throughput format, where the domain, chimeric molecule, sensory receptor protein, or cell or tissue expressing the sensory receptor is attached to a solid phase substrate.

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In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (*e.g.*, the taste transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors,

immunoglobulin receptors and antibodies, the cadherein family, the integrin family, the selectin family, and the like; *see, e.g.,* Pigott & Power, *The Adhesion Molecule Facts Book I* 1993). Similarly, toxins and venoms, viral epitopes, hormones (*e.g.,* opiates, steroids, *etc.*), intracellular receptors (*e.g.,* which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D; peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, poly-amides, polyethyleneimines, polyarylene sulfides, polysiloxanes, polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethelyne glycol) linkers are available from Shearwater Polymers (Huntsville, AL). The linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent which fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups which are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Amino-alkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. *See, e.g.,* Merrifield, *J. Am. Chem. Soc.* 85:2149, 1963 (describing solid phase synthesis of, *e.g.,* peptides); Geysen *et al.*, *J. Immun. Meth.* 102:259, 1987 (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron* 44:6031, 1988 (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al.*, *Science* 251:767, 1991; Sheldon *et al.*, *Clinical Chemistry* 39:718, 1993; and Kozal *et al.*, *Nature Medicine*, 2:753, 1996 (all

describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

4. Computer-based assays

5 Yet another assay for compounds that modulate sensory receptor protein activity involves computer assisted drug design, in which a digital or analog processing system is used to generate a three-dimensional structure of a sensory receptor protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a
10 preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, *e.g.*, ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering
15 protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a sensory receptor polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of those described herein, or fragments or variants thereof.

20 The amino acid sequence represents the primary sequence or subsequence of the protein, which encodes the structural information of the protein. At least 10 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino acids) are entered into the computer system from computer keyboards, computer readable substrates that include, but are not limited to, electronic storage media (*e.g.*,
25 magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM), information distributed by internet sites, and by RAM. The three-dimensional structural model of the protein is then generated by the interaction of the amino acid sequence and the computer system, using software known to those of skill in the art.

The amino acid sequence represents a primary structure that encodes the
30 information necessary to form the secondary, tertiary and quaternary structure of the protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent

accessible surfaces, and hydrogen bonding. Secondary energy terms include van der Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

The tertiary structure of the protein encoded by the secondary structure is then formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the sensory receptor protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of sensory receptor genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used to identify patients having such mutated genes. Identification of the mutated sensory receptor genes involves receiving input of a first nucleic acid or amino acid sequence of a sensory receptor gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once

the first and second sequences are compared, nucleotide or amino acid differences between the sequences are identified. Such sequences can represent allelic differences in various sensory receptor genes, and mutations associated with disease states and genetic traits.

5 5. Cell-based binding assays

In a preferred embodiment, a sensory receptor polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates its maturation and targeting through the secretory pathway. In a preferred embodiment, the heterologous sequence is a rhodopsin sequence, such as an
10 N-terminal fragment of a rhodopsin. Such chimeric sensory receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a functional G protein, *e.g.*, Gal 5, that is capable of coupling the chimeric receptor to an intracellular signaling pathway or to a signaling protein such as phospholipase C. Activation of such chimeric receptors in such cells can be detected
15 using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell.

Activated GPCR receptors become substrates for kinases that phosphorylate the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of ³²P from gamma-labeled GTP to the receptor, which can
20 be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of G-proteins. The kinase/arrestin pathway plays a key role in the desensitization of many GPCR receptors. For example, compounds that modulate the duration an olfactory receptor stays active would be useful as a means of prolonging a desired
25 odor or cutting off an unpleasant one. For a general review of GPCR signal transduction and methods of assaying signal transduction, see, *e.g.*, *Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al.*, *Nature*, 10:349:117-27 (1991); Bourne *et al.*, *Nature*, 348:125-32 (1990); Pitcher *et al.*, *Annu. Rev. Biochem.*, 67:653-92 (1998).

30 Samples or assays that are treated with a potential sensory receptor protein inhibitor or activator are compared to control samples without the test compound, to examine the extent of modulation. Such assays may be carried out in the presence of an odorant that is known to activate the particular receptor, and modulation of the

odorant dependent activation monitored. Control samples (untreated with activators or inhibitors) are assigned a relative sensory receptor activity value of 100. Inhibition of a sensory receptor protein is achieved when the sensory receptor activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of a sensory receptor protein is achieved when the sensory receptor activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electri-cal potential) of the cell or membrane expressing a sensory receptor protein. One means to deter-mine changes in cellular polarization is by measuring changes in current, and thereby measuring changes in polarization, with voltage-clamp and patch-clamp techniques, *e.g.*, the “cell-attached” mode, the “inside-out” mode, and the “whole cell” mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575, 1997). Whole cell currents are conveniently determined using the standard. Other known assays include: assays to measure ion flux using radiolabeled or fluorescent probes such as voltage-sensitive dyes (*see, e.g.*, Vestergarrd-Bogind *et al.*, *J. Membrane Biol.*, 88:67, 1988; Gonzales & Tsien, *Chem. Biol.*, 4:269, 1997; Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185, 1991; Holevinsky *et al.*, *J. Membrane Biology*, 137:59, 1994). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, Northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as Ca^{2+} , IP3, cGMP, or cAMP.

Preferred assays for G-protein coupled receptors include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G-protein coupled receptors as negative or positive controls to assess activity of tested compounds. In assays for identifying modulatory compounds (*e.g.*, agonists,

antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed in the Molecular Probes 1997 Catalog. For G-protein coupled receptors, promiscuous G-proteins such as G α 15 and G α 16 can be used in the assay of choice (Wilkie *et al.*, *Proc. Natl. Acad. Sci.*, 88:10049, 1991). Such promiscuous G-proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*, increases in second messengers such as IP₃, which releases intracellular stores of calcium ions. Activation of some G-protein coupled receptors stimulates the formation of inositol triphosphate (IP₃) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature* 312:315, 1984). IP₃ in turn stimulates the release of intracellular calcium ion stores. Thus, a change in cytoplasmic calcium ion levels, or a change in second messenger levels such as IP₃ can be used to assess G-protein coupled receptor function. Cells expressing such G-protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (see, *e.g.*, Altenhofen *et al.*, *Proc. Natl. Acad. Sci.*, 88:9868, 1991 and Dhallan *et al.*, *Nature* 347:184, 1990). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*, certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors,

serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, sensory receptor protein activity is measured by expressing a sensory receptor gene in a heterologous cell with a promiscuous G-protein that links the receptor to a phospholipase C signal transduction pathway (see Offermanns & Simon, *J. Biol. Chem.*, 270:15175, 1995). Optionally the cell line is HEK-293 (which does not naturally express sensory receptor genes) and the promiscuous G-protein is Gal 5 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by measuring changes in intracellular Ca^{2+} levels, which change in response to modulation of the sensory receptor signal transduction pathway via administration of a molecule that associates with a sensory receptor protein. Changes in Ca^{2+} levels are optionally measured using fluorescent Ca^{2+} indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be measured using immunoassays. The method described in Offermanns & Simon, *J. Biol. Chem.*, 270:15175, 1995, may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159, 1994, may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent No. 4,115,538, herein incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent No. 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing a sensory receptor protein of interest is contacted with a test compound for a sufficient time to

effect any interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent No. 5,436,128, herein incorporated by reference. The reporter genes can be, *e.g.*, chloramphenicol acetyltransferase, luciferase, '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (see, *e.g.*, Mistili & Spector, *Nature Biotech.* 15:961, 1997).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the sensory receptor protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the sensory receptor protein of interest.

6. Transgenic non-human animals expressing sensory receptors

Non-human animals expressing one or more sensory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of translocation domains in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize

odorants/ligands that can bind to a specific or sets of receptors. Such vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, e.g., cell physiology (e.g., on olfactory neurons), on the CNS (e.g., olfactory bulb activity), or behavior.

- 5 Means to infect/express the nucleic acids and vectors, either individually or as libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses.
- 10 When electrodes are located on the olfactory bulb surface it is possible to record stable responses over a period of several days (*see, e.g., Kashiwayanagi, Brain Res. Protoc.* 1:287, 1997). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of
- 15 one turbinate bone or were placed in corresponding positions on four turbinate bones and moved together up toward the top of the bone. *See also, Scott, J. Neurophysiol.* 77:1950, 1997; Scott, *J. Neurophysiol.* 75:2036, 1996; Ezech, *J. Neurophysiol.* 73:2207, 1995. In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and
- 20 medial surface of the turbinates (*see, e.g., Youngentob, J. Neurophysiol.* 73:387, 1995). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g., Khayari, Brain Res.* 539:1, 1991).

- The sensory receptor sequences of the invention can be for example expressed
- 25 in animal nasal epithelium by delivery with an infecting agent, e.g., adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, e.g., Touhara, *Proc. Natl. Acad. Sci. USA* 96:4040, 1999.

- The endogenous olfactory receptor genes can remain functional and wild-type
- 30 (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a “knockout” cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, “gene trap insertion” can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97, 1997). The insertion of the exogenous is typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene’s expression; or a combination thereof. Gene targeting via homologous recombination in pluripotent embryonic stem (ES) cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see* Bijvoet, *Hum. Mol. Genet.* 7:53, 1998); Moreadith, *J. Mol. Med.* 75:208, 1997; Tojo, *Cytotechnology* 19:161, 1995; Mudgett, *Methods Mol. Biol.* 48:167, 1995; Longo, *Transgenic Res.* 6:321, 1997; U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries can also be used as reagents to produce “knockout” human cells and their progeny.

F. Modulators

The compounds tested as modulators of a sensory receptor family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of a sensory receptor gene. Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to screen large chemical libraries by

automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO),
5 Sigma-Aldrich (St. Louis, MO), Fluka Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such
10 “combinatorial chemical libraries” or “ligand libraries” are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional “lead compounds” or can themselves be used as potential or actual therapeutics.

15 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical “building blocks” such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a
20 given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not
25 limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175; Furka, *Int. J. Pept. Prot. Res.* 37:487, 1991; and Houghton *et al.*, *Nature* 354:84, 1991). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (e.g., WO 91/19735), encoded peptides (e.g., WO 93/20242), random bio-oligomers (e.g., WO 92/00091),
30 benzodiazepines (e.g., U.S. Patent No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci.* 90:6909, 1993), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568, 1992), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer.*

Chem. Soc. 114:9217, 1992), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.* 116:2661, 1994), oligo-carbamates (Cho *et al.*, *Science* 261:1303, 1993), peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.* 59:658, 1994), nucleic acid libraries (Ausubel, Berger and Sambrook, all *supra*),
5 peptide nucleic acid libraries (U.S. Patent No. 5,539,083), antibody libraries (Vaughn *et al.*, *Nature Biotechnology* 14:309, 1996 and WO 97/00271), carbohydrate libraries (Liang *et al.*, *Science* 274:1520, 1996) and U.S. Patent No. 5,593,853), small organic molecule libraries (benzodiazepines, Baum, *C&EN*, page 33, Jan 18, 1993); thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pynrolidines, U.S.
10 Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514, and the like.

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS (Advanced Chem Tech, Louisville, KY), Symphony (Rainin, Woburn, MA), 433A (Applied Biosystems, Foster City, CA),
15 9050 Plus (Millipore, Bedford, MA)). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, NJ; Tripos, Inc., St. Louis, MO; 3D Pharmaceuticals, Exton, PA; Martek Biosciences; Columbia, MD; *etc.*).

G. Methods for Representing and Predicting Sensant Perception

20 The invention also preferably provides methods for representing the perception of odor (or taste) and/or for predicting the perception of odor (or taste) in a mammal (*e.g.*, human). Pre-ferably, such methods may be performed by using the receptors and genes encoding the sensory receptors disclosed herein, or fragments or variants thereof.

25 Also provided is a method of screening a chemical sample for the presence of an odor or taste sensed by a mammal (*e.g.*, human), comprising: contacting the chemical sample with one or more of the aforementioned products and detecting binding between sensant ligand and sensory receptor. The sensory receptor, or fragments or variants thereof (*e.g.*, fusion proteins with repor-ters, chimeric proteins)
30 may be expressed in cells; otherwise, ligand-binding domain(s) may be fixed to a substrate (*e.g.*, substantially planar, bead, or fiber) that is solid or porous. The product used in this method is considered a biosensor.

Moreover, a method is provided for simulating a fragrance or flavor sensed by a mammal (*e.g.*, human), comprising: for each of a plurality of sensory receptors, or fragments or variants thereof, ascertaining the extent to which the sensory receptor interacts with the fragrance and/or flavor; and combining a plurality of compounds, each having a previously-determined interaction with one or more of the sensory receptors, in amounts that together provide a stimulation profile that mimics the profile for the fragrance and/or flavor. Interaction of a fragrance and/or flavor with a sensory receptor can be determined using any of the binding or reporter assays described herein. The interactions can be aggregated or a profile generated using known signal processing techniques (*e.g.*, a neural network) as described below. The sensory receptor, or fragments or variants thereof (*e.g.*, fusion proteins with reporters, chimeric proteins) may be expressed in cells; otherwise, ligand-binding domain(s) may be fixed to a substrate (*e.g.*, planar, bead, or fiber) that is solid or porous. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80%, 90%, 95%, 99% or all of the receptors that are substantially stimulated by the fragrance or flavor.

In yet another aspect of the invention, a method is provided in which a plurality of standard compounds are tested against a plurality of sensory receptors, or fragments or variants thereof, to ascertain the extent to which the sensory receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on data storage medium. The method may further comprise providing a desired receptor-stimulation profile for an odor and/or taste; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the odor and/or taste.

A further aspect of the invention is to provide a method for representing sensory perception of a particular odor and/or taste in a mammal (*e.g.*, human), comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is greater than or equal to 5, n is

greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; and generating from the values a quantitative representation of sensory perception. The sensory receptors may be a receptor disclosed herein, or fragments or variants thereof. The representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, or may constitutes a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced sensory receptors, or fragments or variants thereof, with a composition and quantitatively measuring the interaction of the composition with the receptors. The maximum number of taste receptors that are needed to mimic the native repertoire (*e.g.*, about 50) may be less than the maximum number of olfactory receptors that are needed (*e.g.*, about 350). But the number of sensory receptors that need to be represented in an assay to provide useful results may be much less.

It is yet another aspect of the invention to provide a method for predicting the sensory perception in a mammal (*e.g.*, human) generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in the mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is greater than or equal to 5, n is greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; for one or more molecules or combinations of molecules yielding known sensory perception in a mammal; and generating from the values a quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding known sensory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is

greater than or equal to 5, n is greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; for one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal; and generating from the values a quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal by comparing the quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal to the quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding known sensory perception in a mammal. The sensory receptors used in this method may include a receptor disclosed herein, or fragment or variant thereof. The maximum number of taste receptors that are needed to mimic the native repertoire (*e.g.*, about 50) may be less than the maximum number of olfactory receptors that are needed (*e.g.*, about 350). But the number of sensory receptors that need to be represented in an assay to provide useful results may be much less.

Assaying for ligand-receptor binding in a large set of sensory receptors is envisioned to mimic the function of the nose or tongue in sensory perception of chemical sensants. For a set of sensory receptors with a redundancy of ligand-binding domains, the resultant signal is a summation of the interactions of all sensory receptors in the set: none, one, or a few of which have ligand-binding domains that are a perfect fit for the sensant; some of which have ligand-binding domains that are only an imperfect fit for the sensant; and most of which do not significantly bind to the sensant. The individual sensory receptor's binding affinity for sensant varies accordingly. Thus, a suitably large set of ligand-binding domains from sensory receptors will be analogous to any ability of the native repertoire of olfactory or taste receptors to tolerate varying degrees of mismatch between ligand and ligand-binding domain.

The complication of desensitization of sensory receptor signaling will also be avoided by using the invention instead of preparations of nasal or tongue epithelium containing native sensory receptors. For example, the event of binding between ligand and receptor can be separated from more complicated downstream signaling events in the epithelial cells. But the latter events can be reconstituted in the invention by transferring the sensory receptor of interest into appropriate host cells containing an intact and functional signaling pathway.

H. Administration of Novel Sensant Compositions

Sensory modulators can be administered directly to a mammal (*e.g.*, human) for modulation of sensory perception *in vivo*. Administration is by any of the routes normally used for introducing a modulator compound into ultimate contact with the tissue to be treated (*e.g.*, nose or tongue). The olfactory modulators are administered in any suitable manner, optionally with acceptable carriers. Suitable methods of administering such modulators are available and well known to those of skill in the art, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route. Acceptable carriers are determined at least in part by the particular components of the composition to be administered (*e.g.*, stabilizing the sensants), as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions of the present invention (*see, e.g., Remington's Pharmaceutical Sciences*, 17th ed. 1985).

The sensory modulators, alone or in combination with other suitable components, can be made into aerosol formulations (*i.e.*, they can be "nebulized") to be administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichloro-difluoromethane, propane, nitrogen, and the like that may or may not contribute to sensory perception. Other possible formulation include dry or liquid forms, powders or tablets, solutions of polar (*e.g.*, water) or nonpolar (*e.g.*, alcohol) solvents, emulsions or suspensions, creams, gels, lotions, and syrups.

Formulations suitable for administration include aqueous and non-aqueous solutions, isotonic sterile solutions, which can contain antioxidants; buffers,

bacteriostats, and solutes that render the formulation isotonic, and aqueous and non-aqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. In the practice of this invention, compositions can be administered, for example, by orally, topically, intravenously, intraperitoneally, intravesically, or intrathecally. Optionally, the compositions are administered orally or nasally. The formulations of compounds can be presented in unit-dose or multi-dose sealed containers, such as ampules and vials. Solutions and suspensions can be prepared from sterile powders, granules, and tablets of the kind previously described. The modulators can also be administered as part of prepared drug, food, or cosmetic. In particular, an unpleasant odor or taste (*e.g.*, sulfur or bitter, respectively) may not be perceived as such and/or its effects reduced by blocking the binding between sensant ligand and sensory receptor by adding a competitor ligand that blocks binding between cognate ligand and receptor, or inhibiting or reducing signal transduction. In contrast, a pleasant odor or taste can be mimicked or enhanced. Primary sensants are preferred because the subset of activated cells is kept small and the effects limited to projection into a specific region of the brain. But novel olfactants or combinations thereof that bind only a few olfactory receptors (*e.g.*, having less than five different ligand-binding domains) would also be useful.

The dose administered to a mammal (*e.g.*, human) should be sufficient to effect a beneficial response in the subject over time. The dose will be determined by the efficacy of the particular sensory modulators employed and the condition of the subject, as well as the body weight or surface area of the area to be treated. The size of the dose also will be determined by the existence, nature, and extent of any adverse side-effects that accompany the administration of a particular compound or vector in a particular subject. In determining the effective amount of the modulator to be administered in a physician may evaluate circulating plasma levels of the sensory modulator, modulator toxicities, and the production of anti-modulator antibodies. In general, the dose equivalent of a modulator is from about 1 ng/kg to 10 mg/kg for the typical mammal. For administration, sensory modulators can be administered at a rate determined by the ED₅₀ of the modulator, and the side-effects of the inhibitor at various concentrations, as applied to the mass and overall health of the mammal. Administration can be accomplished via single or divided doses.

I. Kits

Sensory receptor genes, or fragments or variants thereof are useful tools for identifying cells expressing sensory receptors, for forensics and paternity determinations, and for examining signal transduction in isolated cells. Sensory receptor family member-specific reagents that specifically hybridize to sensory receptor nucleic acids, such as AOFLF1 probes and primers, and sensory receptor specific reagents that specifically bind to a sensory receptor protein, *e.g.*, anti-sensory receptor antibodies are used to examine expression in cells and regulation of signal transduction. For example, one or more family member-specific reagents may be used to detect poly-morphisms that are linked to genetic anosmia or to detect allelic exclusion.

Nucleic acid assays for the presence of DNA and RNA for a sensory receptor family member in a sample include numerous techniques are known to those skilled in the art, such as Southern analysis, Northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such as to be available for hybridization within the cell while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*, *Biotechniques*, 4:230-250 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, a sensory receptor protein can be detected with the various immunoassay techniques described above. The test sample is typically compared to both a positive control (*e.g.*, a sample expressing a recombinant sensory receptor protein) and a negative control.

The present invention also provides for kits for screening for novel modulators of sensory receptor family members. Such kits can be prepared from readily available materials and reagents, as well as any of the aforementioned products. For example, such kits can comprise any one or more of the following materials: sensory receptor nucleic acids or proteins, reaction tubes, and instructions for testing sensory receptor activity. Optionally, the kit contains a biologically active sensory receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

Examples

AOLFR1 sequences:

MKTFSSFLQIGRNMHQGNQTTITEFILLGFFKQDEHQNLLFVFLGMYLVTVIGNGLIIVAISLD
TYLHTPMYLFANLSFADISSISNSVPKMLVNIQTKSQSISYESCITQMYFSIVFVIDNLLGTM
5 AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIALTHLLLIQLLFCNHNTLPHFCDLAPLL
KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCIIRAVLRVSSTQGKWKAFTSCGSHLTVVLLFY
GTIVGVYFFPSSTHPEDTDKIGAVLFTVVTMNPFIYSLRNKDMKGALRKLINRKISSL (SEQ ID
NO: 1)

10 ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA
CCATCACTGAATTCATTCTCCTGGGATTTTCAAGCAGGATGAGCATCAAAACCTCCTCTTT
GTGCTTTTCTTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATCATTGTGGCTA
TCAGCTTGATACGTACCTTCATACCCCCATGTATCTCTCCTTGCCAATCTATCCTTTGCT
GATATTTCTCCATTTCCTCACTCAGTCCCCAAAATGCTGGTGAATATTCAAACCAAGAGTC
15 AATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTTCTATTGTGTTTGTGCTCATT
GACAATTTGCTCTTGGGGACCATGGCCTATGACCACCTTTGTGGCGATCTGCCACCCCTCTGA
ATTATACAATTCTCATGCGGCCAGGTTGCGCATTTTGTCTCACAGTCATCTCATGGTTCCTC
AGTAATATTATTGCTCTGACACACACCCTTCTGCTCATTCAATTGCTCTTCTGTAACCACAA
CACTCTCCACACTTCTTCTGTGACTTGGCCCCTCTGCTCAAAGTGTCTGTTTCAGATACAT
20 TGATCAATGAGCTTGTGTTGTTTATTGTGGGTTTATCAGTTATCATCTTCCCCTTTACACTC
AGCTTCTTTTCTATGTCTGCATCATCAGAGCTGTCTGAGAGTATCTTCCACACAGGGAA
AGTGGAAGCCTTCTCCACTTGTGGCTCTCACCTGACAGTTGTATTACTGTTCTACGGAAC
CATTGTAGGCGTGTACTTTTCCCCTCCTCCACTCACCTGAGGACACTGATAAGATTGGT
GCTGTCTATTCACTGTGGTGACACCCATGATAAACCCCTTCATCTACAGCTTGAGGAATA
25 AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTTCTTCCCCTTTGA (SEQ
ID NO: 2)

AOLFR2 sequences:

MMVLRNLSMEPTFALLGFTDYPKLQIPLFLVFLMYVITVVGNLGMIIIIKINPKFHTPMYFFL
30 SHLSFVDFCYSSIVTPKLENLVMADKSIFYFSCMMQYFLSCTAVVTESFLLAVMAYDRFVAIC
NPLLYTVAMSQRLLCALLVAGSYLWGMFGPLVLLCYALRLNFSGPNVINHFFCEYALISVSGS
DILIPHLLLSFATFNEMCTLLIILTSYVFIFVTVLKIRSVSGRHKAFSTWASHLTAITIFHGTLFL
YCVPSNKSNSRQTVKVASVFYTVVNPMLNPPIYSLRNKDVKDAFWKLIHTQVPFH (SEQ ID NO:
3)

35 ATGATGATGGTTTTAAGGAATCTGAGCATGGAGCCCACCTTTGCCCTTTTAGGTTTCACAG
ATTACCCAAAGCTTCAGATTCCTCTCTTCTTGTGTTTCTGCTCATGTATGTTATCACAGTG
GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAAACCCAAATTCACACTCCTATGT
ACTTTTTCTTAGTCACCTCTCTTTTGTGATTGTTTGTACTCTTCCATTGTCACCTCCCAAGC
40 TGCTTGAGAACTTGGTAATGGCAGATAAAAGCATCTTCTACTTTAGCTGCATGATGCAGTA
CTTCTGTCTGCACTGCTGTGGTGACAGAGTCTTTCTGCTGGCAGTGATGGCCTATGAC
CGCTTTGTGGCCATCTGCAATCCTCTGCTTTATACAGTGGCCATGTCACAGAGGCTCTGTG
CCCTGCTGGTGGCTGGGTCATATCTCTGGGGCATGTTTGGCCCCTTGGTACTCCTTTGTTAT
GCTCTCCGGTTAAACTTCTCTGGACCTAATGTAATCAACCACTTCTTTTGTGAGTATACTGC
45 TCTCATCTCTGTGCTGGCTCTGATATACTCATCCCCACCTGCTGCTTTTCAGCTTCGCCA
CCTTCAATGAGATGTGTACACTACTGATCATCCTCACTTCCATGTTTTCATTTTTGTGACT
GTACTAAAAATCCGTTCTGTAGTGGGCGCCACAAAGCCTTCTCCACCTGGGCCTCCCACC
TGACTGCTATCACCATCTTCCATGGGACCATCCTTTTCTTTACTGTGTACCCAACTCCAAA
AACTCTCGGCAACAGTCAAAGTGGCCTCTGTATTTTACACAGTTGTCAACCCCATGCTGA
50 ACCCTCCGATCTACAGCCTAAGGAATAAAGACGTGAAGGATGCTTTCTGGAAGTTAATACA
TACACAAGTTCCATTTCACTGA (SEQ ID NO: 4)

AOLFR3 sequences:

MLLTDRNTSGTTFLLGFSDYPELQVPLFLVFLAIYNVTVLGNIGLIVIIKINPKLHTPMYFFLSQ
55 LSFVDFCYSSIIAPKMLVNLVVKDRITISFLGCVVQFFFFCTFVVTESFLLAVMAYDRFVAICNPL
LYTVDMSQLCLVLLVVGSYAWGVSCSLELTCSALKLCFHGFNTINHFFCFESSLLSLSCSDTYI

NQWLLFFLATFNEISTLLIVLTSYAFIVVTILKMRSVSGRRKAFSTCASHLTAITIFHGTLFLYCV
PNSKNSRH TVKVASFYTVVIPMLNPLIYSLRNKDVKDTVTEILD TKVFSY (SEQ ID NO: 5)

5 ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTACCCTCTTGGGCTTCTCAGATT
ACCCAGAACTGCAAGTCCCACTCTTCCTGGTTTTCTGGCCATCTACAATGTCAGTGTGCTA
GGGAATATTGGGTTGATTGTGATCATCAAAATCAACCCCAAACCTGCATACCCCATGTACT
TTTCCTCAGCCAACTCTCCTTTGTGGATTCTGCTATTCTCCATCATTGCTCCCAAGATG
TTGGTGAACCTTGTGTCAAAGACAGAACCATTTCATTTTTAGGATGCGTAGTACAATTCT
TTTTCTTCTGTACCTTTGTGGTCACTGAATCCTTTTTATTAGCTGTGATGGCCTATGACCGC
10 TTCGTGGCCATTGCAACCCTCTGCTCTACACAGTTGACATGTCCAGAACTCTGCGTGC
TGCTGGTTGTGGGATCCTATGCCTGGGGAGTCTCATGTTCTTGGAAGTACGCTGCTCTGC
TTTAAAGTTATGTTTCATGGTTTCAACACAATCAATCACTTCTTCTGTGAGTTCTCCTCAC
TACTCTCCCTTTCTTGCTCTGATACTTACATCAACCAGTGGCTGCTATTCTTTCTTGCCACC
TTAATGAAATCAGCACACTACTCATCGTTCTCACATCTTATGCGTTCATTGTTGTAACCAT
15 CCTCAAGATGCGTTCAGTCAGTGGGCGCCGCAAAGCCTTCTCCACCTGTGCCTCCCACCTG
ACTGCCATCACCATCTTCCATGGCACCATCCTCTTCCTTTACTGTGTGCCAACTCCAAAA
CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCATGTTGAAT
CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC
ACCAAAGTCTTCTTACTGA (SEQ ID NO: 6)

20

AOLFR4 sequences:

MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLS
LLDVMFSSV VAPKVVDTL SKSTTISLKGCLTQLFVEHFFGGVGHILLTVMAYDRYVAICKPLHY
TIIMSPRVCCLMVGGAWVGGFMHAMIQLLFMYQIPFCGPNIDHFI CDLFQLLTLACTDTHILGL
25 LVTNLNGMMCVAIFLILIASYTVILCSLSYSSKGRHKALSTCSSHLTVVVLFFVPCIFLYMRPV
VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

ATGGAAAATCAAAACAATGTGACTGAATTCATTCTTCTGGGTCTCACAGAGAACCTGGAGC
TGTGGAAAATATTTTCTGCTGTGTTTCTTGTCATGTATGTAGCCACAGTGTGGAAAATCT
30 ACTTATTGTGGTAACTATTATCACAAGTCAGAGTCTGAGGTCACCTATGTATTTTTCTTA
CCTTCTTGTCCTTTTGGATGTCATGTTCTCATCTGTGCTTGCCCCCAAGGTGATTGTAGAC
ACCTCTCCAAGGACTACTCATCTCTCTCAAAGGCTGCCTCACCCAGCTGTTTGTGGAGC
ATTTCTTTGGTGGTGTGGGGATCATCCTCCTCACTGTGATGGCCTATGACCGCTACGTGGC
CATCTGTAAGCCCCTGCACTACACGATCATCATGAGTCCACGGGTGTGCTGCCTAATGGTA
35 GGAGGGGCTTGGGTGGGGGATTTATGCACGCAATGATACAACCTTCTTTCATGTATCAAA
TACCCTTCTGTGGTCTTAATATCATAGATCACTTTATATGTGATTTGTTTCAGTTGTTGACA
CTTGCTGCACGGACACCCACATCCTGGGCCTCTTAGTTACCCTCAACAGTGGGATGATGT
GTGTGGCCATCTTTCTTATCTTAATTGCGTCCTACACGGTCATCCTATGCTCCCTGAAGTCT
TACAGCTCTAAAGGGCGGCACAAAGCCCTCTTACCTGCAGCTCCCACCTCACGGTGGTTG
40 TATTGTTCTTTGTCCCCTGTATTTCTTGTACATGAGGCCTGTGGTCACTCACCCATAGAC
AAGGCAATGGCTGTGTGCACTCAATCATCACCCCATGTTAAATCCCTTGATCTATACAC
TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAACTCTGGATGAAATGGGAGGCTTTGG
CTGGGAAATAA (SEQ ID NO: 8)

AOLFR5 sequences:

MGKENCTTVAEFILLGLSDVPELRVCLFLLFLLIYGVTL LANLGMIALIQVSSRLHTPMYFFLSH
LSSVDFCYSSIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLLAVMAYDRFVAICNPL
LYTVTMSWKVRVELASCCYFCGTVC SLIHLCLALRIPFYRSNVINHFFCDLPPVLSLACSDITVN
ETLLFLVATL NESVTIMILTSYLLILTILKMGS AEGRHKAFSTCASHLTAITVFHGTVLSIYCRP
50 SSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKEALRKVMGSKIHS (SEQ ID NO: 9)

ATGGGCAAGGAAAACCTGCACCACTGTGGCTGAGTTCATTCTCCTTGGACTATCAGATGTCC
CTGAGTTGAGAGTCTGCCTCTTCCTGCTGTTCTTCTCATCTATGGAGTCACGTTGTTAGCC
AACCTGGGCACTGATTGCAGTATTGAGTCACTCTCGGCTCCACACCCCATGTAATTTT
55 TCCTCAGCCACTGTCTCTGTAGATTTCTGCTACTCCTCAATAATTGTGCCCCAAAATGTTG
GCTAATATCTTTAACAAGGACAAAGCCATCTCCTTCTAGGGTGCATGGTGCAATCTACT

TGTTTTGCACCTTGTGTGGTCACTGAGGTCTTCCTGCTGGCCGTGATGGCCTATGACCGCTTT
 GTGGCCATCTGTAACCCCTTTGCTATACACAGTCACCATGTCTTGGAAGGTGCGTGTGGAGC
 TGGCTTCTTGCTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCAATTTGTGCTTAGCTCTT
 AGGATCCCCCTTCTATAGATCTAATGTGATTAACCACTTTTTCTGTGATCTACCTCCTGTCTT
 5 AAGTCTTGCTTGCTCTGATATCACTGTGAATGAGACACTGCTGTTCTGGTGGCCACTTTG
 AATGAGAGTGTTACCATCATGATCATCCTCACCTCCTACCTGCTAATTCTCACCACCATCCT
 GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCCACCTCACA
 GCTATCACTGTCTTCCATGGAACAGTCCTTCCATTTATTGCAGGCCAGTTCAGGCAATA
 GTGGAGATGCTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCCCTATGCTGAATC
 10 TGTGATCTACAGCCTGAGAAATAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC
 CAAAATTCACCTCCTAG (SEQ ID NO: 10)

AOLFR6 sequences:

15 MMASERNQSSTPTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMYFFLS
 HSLTDFCFSTVVPKLEENLVVEYRTISFSGCIMQFCFACIFGVTEFMLAAMAYDRFVAVCK
 PLYTTIMSQKLCALLVAGSYTWGIVCSLILTYFLDLSCFESTFINNFICDHSVIVSASYSDPYIS
 QRLCFIIAIFNEVSSLIILTSYMLIFTTIMKMRSASGRQKTFSTCASHLTAITIFHGTLFLYCVPNP
 KTSSLIVTVASVFYTVAIPLMLNPLIYSLRNKDINNMFEKLVVTKLIYH (SEQ ID NO: 11)

20 ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTTGGGTTTTTTCAG
 AATACCCAGAAATCCAGGTTCCACTCTTCTGGTTTTCTTGTTCTGCTACACAGTCACTGTA
 GTGGGGAACCTTGGGCATGATAATAATCATCAGACTCAATTCAAAACCTCATACAATCATGT
 ACTTTTTCTTAGTCACTTGCTTGCCTTGACAGACTTCTGTTTTTCCACTGTAGTTACACCTAAA
 CTGTTGGAGAACTTGGTTGTGGAATACAGAACCATCTCTTCTCTGGTTGCATCATGCAAT
 25 TTTGTTTTGCTTGCATTTTGGAGTGACAGAACTTTCATGTTAGCAGCGATGGCTTATGAC
 CGTTTTGTGGCAGTTTGTAACCCCTTGCTGTATACCACTATTATGTCTCAGAAGCTCTGTGC
 TCTTCTGGTGGCTGGGTCCCTATACATGGGGGATAGTGTGCTCCCTGATACTCACATATTTT
 CTTCTTGACTTATCGTTTTGTGAATCTACCTTCATAAATAATTTTATCTGTGACCACTCTGT
 AATTGTTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTATTATTGCCA
 30 TATTCAATGAGGTGAGCAGCCTAATTATCATTTCTGACATCATATATGCTTATTTTCACTACC
 ATTATGAAGATGCGATCTGCAAGTGGGCGCCAGAAAACCTTCTCCACCTGTGCCTCCCACC
 TGACAGCCATCACTATCTTCCATGGAACCTATCCTTTTCTTTACTGTGTTCCTAATCCTAAA
 ACTTCTAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGCTGA
 ACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTTGT
 35 CACCAAATTGATTTACCACTGA (SEQ ID NO: 12)

AOLFR7 sequences:

40 MSYFYRLKLMKEAVLVKLPFTSLPLLQTLRKSRLDMEIKNYSSSTSGFILLGLSSNPQLQKPLF
 AIFLIMYLLAAVGNVLIIPAIYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFSETKVISY
 VGCLAQMYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSISHLHSL
 FRVLLMSRLSFCASHIIKHFFCDTQPVLKLSGSDTSSSQMVVMTETLAVIVTPFLCIIFSYLIMV
 TVLRIPSAAGKWKAFTSCGSHLTAVALFYGSIIYVYFRPLSMYSVVRDRVATVMYTVVTPMLN
 PFIYSLRNKDMKRGLKKLQDRIYR (SEQ ID NO: 13)

45 ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACCTGCCCTTCA
 CATCTCTCCCACTGCTTCTCCAAACCCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA
 CTACAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCAACCCCTCAGCTGCAG
 AAACCTCTCTTTGCCATCTTCCCTCATCATGTACCTGCTCGCTGCGGTGGGGAATGTGCTCAT
 CATCCCGGCCATCTACTCTGACCCCAAGGCTCCACACCCCTATGTACTTTTTTCTCAGCAACT
 50 TGTCTTTCATGGATATCTGCTTCAACAGTCATAGTGCCTAAGATGCTGGTGAATTTTCTA
 TCAGAGACAAAGGTTATCTCCTATGTGGGCTGCCTGGCCAGATGTACTTCTTTATGGCAT
 TTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCGGCTGGTGGCCATCTG
 CAACCCCTTACACTATGATGTGGTTATGAAACCACGGCATTGCCTGCTCATGCTATTGGGT
 TCTTGACGATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTATGTCTCGCTTGTCTTT
 55 CTGTGCCTCTCACATCATTAAGCACTTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT
 GCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTTAGCTGTCATTGTGAC

5 CCCCTTCCTGTGTATCATCTTCTCCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCCCT
CTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCCACTCACTGCAGTAGCCCT
TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCCGTGCCATGTACTCAGTGGTTAGGG
ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCTTTCATCTACAG
CCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAATTTACCGGTA
A (SEQ ID NO: 14)

AOLFR8 sequences:

10 MATSNHSSGAEFILAGLTQRPELQLPLFLLFLGIYVTVVGNLGMIFLIALSSQLYPPVYYFLSH
LSFIDLCYSSVITPKMLNMFVPEENIISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRPLLY
NIVMSHRVCSIMMAVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTLSCSSTHINEI
LLFIIGGVNTLATTALVLISYAFIFSSILGIHSTEGQSKAFGTCSHLLAVGIFFGSITFMYFKPPSS
TTMEKEKVSSVFYITIIPMLNPLIYSLRNKDVKNALKKMTRGRQSS (SEQ ID NO: 15)

15 ATGGCTACTTCAAACCATTCTTCAGGGGCTGAGTTTATCCTGGCAGGCTTGACACAACGCC
CAGAACTTCAACTGCCACTCTTCCTCCTGTTCTTGGAATATATGTGGTCACAGTGGTGGG
GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTTACCTCCAGTGTATTATT
TTCTCAGTCATTTGTCTTTTATTGATCTCTGCTACTCCTCTGTCATTACCCCTAAGATGCTG
GTGAACTTTGTTCCAGAGGAGAACATTATCTCCTTTCTGGAATGCATTACTCAACTTTATTT
20 CTTCTTATTTTTGTAATTGCAGAAGGCTACCTTCTGACAGCCATGGAATATGACCGTTAT
GTTGCTATCTGTCGCCCCTGCTTTACAATATTGTCATGTCCACAGGGTCTGTTCCATAAT
GATGGCTGTGGTATACTCACTGGGTTTTCTGTGGGCCACAGTCCATACTACCCGCATGTCA
GTGTTGTCATTCTGTAGGTCTCATACGGTCAGTCATTATTTTTGTGATATTCTCCCCTTATT
GACTCTGCTTGTCTCCAGCACCCACATCAATGAGATTCTGCTGTTTATTGAGGAGTT
25 AATACCTTAGCAACTACACTGGCGGTCCTTATCTCTTATGCTTTTCTCTAGTATCCT
TGGTATTCATTCCACTGAGGGGCAATCCAAAGCCTTTGGCACTTGTAGCTCCCATCTCTTG
GCTGTGGGCATCTTTTTTGGGTCTATAACATTGATGATTTCAAGCCCCCTTCCAGCACTAC
TATGGAAAAAGAGAAGGTGTCTTCTGTGTTCTACATCACAATAATCCCCATGCTGAATCCT
CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA
30 AGGCAGTCATCCTGA (SEQ ID NO: 16)

AOLFR9 sequences:

35 MLARNNSLVTEFILAGLTDRPEFWQPFFFLFLVIYIVTMVGNLGLITLFLGLNSHLHTPMYYFLFN
LSFIDLCYSSVFTPKMLNMFVSKKNISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL
LYKVTMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANIINHLYLCDILPLLQLSCTSTYV
NEVVVLIVVGTNITVPSCILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAAFMYIKY
SSGSMEQGVFSVFYTNVPMNLPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 17)

40 ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
CAGAGTTCTGGCAACCTTCTTTTTCTGTTCTAGTGATCTACATTGTCACCATGGTAGGC
AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT
GAACTTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC
45 TTTCTCTTTTTTCGTCATCTCTGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT
GGCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCA
CTTTTGCTGTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGTTTAG
ACTCACCTTCTGCAGTGCTAATATCATTAACCATTACTTGTGTGACATACTCCCCCTCCTCC
AGCTTTCTGCAACCAGCACCTATGTCAACGAGGTGGTGTCTCATTGTTGTGGGTACTAA
TATCACGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTTATTGTCACTAGCATCTTC
50 ATATCAAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGCTATTGC
TCTGTCTCTGTTTTTGGGTGAGCGGCATTGATGATATTAATAATTCTTCTGGATCTATGG
AGCAGGAAAAAGTTTTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCCCCTCATC
TACAGGTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTCAG
AGGAGAAATATATTCTAA (SEQ ID NO: 18)

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ATGGAAAGAAACCACAATCCAGATAATTGTAATGTTTTAAATTTTTCTTTGCTGATAAGA
AGAATAAAAGGAGAAATTTTGGACAGATTGTATCAGATGTTGGAAGAATCTGTTACAGTG
TTAGTTTATCTTTAGGTGAACCCACAATATGGGAAGAAATAACCTAACAAGACCCTCTGA
ATTCATCCTCCTTGGACTCTCCTCTCGACCTGAGGATCAGAAGCCGCTCTTTGCTGTGTTCC
5 TCCCCATCTACCTTATCACAGTGATAGGAAACCTGCTTATCATCCTGGCCATCCGCTCAGA
CACTCGTCTCCAGACGCCCATGTACTTCTTTCTAAGCATCCTGTCTTTTGTGACATTGCT
ATGTGACAGTCATTATCCCTAAGATGCTGGTGAACCTTCTTATCAGAGACAAAGACCATCTC
TTACGGTGAGTGTCTGACCCAGATGTACTTTTCTTAGCCTTTGGAAACACAGACAGTTAC
CTGCTAGCAGCCATGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCACTACATCA
10 CCATTATGAGTCACAGATGCTGTGCTCTGCTTCTGGTTCTCTCCTTCTGCATTCCACATTTT
CACTCCCTCCTGCACATTCTTCTGACTAATCAGCTCATCTTCTGTGCCTCCAATGTCATCCA
TCACTTTTTCTGCGATGATCAACCAGTGCTAAAATTGCTCTGTTCCCTCCCATTTTGTCAAAG
AAATCACAGTAATGACAGAAGGCTTGGCTGTCATAATGACCCCGTTTTTCATGCATCATCAT
CTCTTATTTAAGAATCCTCATCACTGTTCTGAAGATTCTTCAGCTGCTGGAAAGCGTAAA
15 GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCTGTTTTATGGAAGCATTAGCTA
TGTCTATTTTACAGCCCCTGTCCAATACTGTCAAGGATCAAATAGCAACAATTATCTAC
ACCGTACTGACTCCTATGCTAAATCCATTTATCTATAGTCTGAGGAACAAAGACATGAAGC
AGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

20 **AOLFR13 sequences:**

MDQKNGSSFTGFILLGFSDRPQLELVLFVLLIFYIFTLLGNKTIIVLSHLDPHLHNPMYFFFSNL
SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLGSTECVLLGVMAFDRYAAVCRPL
HYTVVMHPCLYVLMASWSVIGFANSLLQTVLILLTLCGRNKLEHFLCEVPPLKLACVDTT
MNESEFFVSVIIIIVPVALIIFSYSQIVRAVVRISATGQRKVFGTCGSHLTVVSLFYGTAIYAY
25 LQPGNNYSQDQGXISLFYTIITPMINPLIYTLRNKDVKGALKKVLWKNYDSR (SEQ ID NO:
25)

ATGGATCAGAAAAATGGAAGTTCTTTCACTGGATTTATCCTACTGGGTTTCTCTGACAGGC
CTCAGCTGGAGCTAGTCCTCTTTGTGGTTCTTTGATCTTCTATATCTTCACCTTGTGGGG
30 AACAAAACCATCATTGTATTATCTCACTTGGACCCACATCTTCACAATCCTATGTATTTTT
CTTCTCCAACCTAAGCTTTTTGGATCTGTGTTACACAACCGGCATTGTTCCACAGCTCCTGG
TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGTAGTTCAGCTGTACAT
CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTGACCGCTAT
GCAGCTGTTTGCAGGCCCCCTCCACTACACAGTAGTCATGCACCCTTGTCTGTATGTGCTGA
35 TGGCTTCTACTTCATGGGTCAATTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTG
CTTTTAACACTTTGTGGAAGAAATAAATTAGAACACTTTCTTTGTGAGGTTCCCTCCATTGCT
CAAGCTTGCCTGTGTTGACACTACTATGAATGAATCTGAACTCTTCTTTGTGAGTGTCATTA
TTCTTCTTGTACCTGTTGCATTAATCATATTCTCCTATAGTCAGATTGTCAGGGCAGTCGTG
AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTTTGGGACATGTGGCTCCCACCTCACA
40 GTGGTTTTCCCTGTTCTACGGCACAGCTATCTATGCTACCTCCAGCCCGCAACAATACTC
TCAGGATCAGGGCAAGKTCATCTCTCTCTTCTACACCATCATTACCCCATGATCAACCCC
CTCATATATACACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG
AACTACGACTCCAGATGA (SEQ ID NO: 26)

45 **AOLFR14 sequences:**

MALPLLLSPSCFASSQSLSSRMNSENLTAAVAPAEFVLLGITNRWDLRVALFLTCLPVYLVSL
LGNMGMAILLIRMDARLHTPMYFFLANLSLLDACYSSAIGPKMLVDLLLPRATIPYTACALQMF
VFLAGLADTECLLAAMAYDRYVAIRNPLLYTTAMSQRLCLALLGASGLGGAVSAFVHTTLTF
RLSFCRSRKINSFFCDIPLLAISCSDTSLNELLFAICGFIQTATVLAITVSYGFIAGAVIHMRSVE
50 GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSSYALDTDKMASVFYTLVIPSLNPLIYSLRKE
VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCTCTTCTCAGTCTCTGTCCAGTAG
GATGAACTCAGAGAACCTCACCCGGGCGCGGTTGCCCTGCTGAATTGCTCCTCCTGGGC
55 ATCACAAATCGCTGGGACCTGCGTGTGGCCCTCTTCTGACCTGCCTGCCTGTCTACCTGG
TGAGCCTGCTGGGAAACATGGGCATGGCGCTGCTGATCCGCATGGATGCCCGGCTCCACA

5 CACCTATGTACTTCTTCCTGGCCAACCTCTCCCTGCTGGATGCCTGCTATTCCTCCGCCATC
GGCCCCAAGATGCTAGTGGACCTGCTGCTGCCCCGAGCCACCATCCCTTACACAGCCTGTG
CCCTCCAGATGTTTGTCTTTGCAGGTCTGGCTGATACTGAGTGTGCTTGCTGGCAGCCAT
GGCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATAACAACAGCTATGTGCGAG
10 CGTCTATGCCTGGCCTTGCTGGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGCCTTTGTTC
ACACAACCTCACCTTCCGCCTGAGCTTCTGCCGCTCCCGGAAGATCAATAGCTTCTTCTG
CGATATCCCTCCACTGCTGGCCATCTCGTGCAGTGACACCAGTCTCAATGAACCTCTTCTCT
TCGCCATCTGTGGCTTCATCCAGACAGCCACGGTGTTAGCTATCACGGTGTCTTATGGCTT
CATCGCTGGGGCTGTGATCCACATGCGCTCGGTTCGAGGGCAGTCGGCGAGCAGCCTCCAC
15 CGGTGGTTCCACCTCACAGCCGTGGCCATGATGTACGGGACACTCATTTTTCATGTACCTG
CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCTGG
TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT
CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGGTCCCAGTGA (SEQ ID NO: 28)

15 **AOLFR15 sequences:**

MRENNQSSSTLEFILLGVTGQQEQEDFFYILFLFIYPITLIGNLLIVLAICSDVRLHNP MYFLANLS
LVDIFFSSVTIPKMLANHLLGSKSISFGGCLTQMYFMIALGNTDSYILAAMAYDRAVAISHPLH
YTTIMSPRSCIWLIAGSWVIGNANALPHTLLTASLSFCGNQEVANFYCDITPLKLSCSDIHFHV
20 KMMYLGVGIFSVPLLCIIVSYIRVFSTVFQVPSTKGVLKAFSTCGSHLTVVSLYYGTVMGTYFR
PLTNYSLKDAVITVMYTA VTPMLNPFYISLRN RDMKAALRKLFNKRISS (SEQ ID NO: 29)

25 ATGAGGGAAAATAACCAGTCCTCTACACTGGAATTCATCCTCCTGGGAGTTACTGGTCAGC
AGGAACAGGAAGATTTCTTCTACATCCTCTTCTGTTTACATTTACCCCATCACATTGATTGGA
AACCTGCTCATTGTCTAGCCATTTGCTCTGATGTTTCGCCTTACAAACCCCATGTATTTTCT
CCTTGCCAACCTCTCCTTGGTTGACATCTTCTCTCATCGGTAACCATCCCTAAGATGCTGG
CCAACCATCTCTTGGGCAGCAAATCCATCTCTTTTGGGGGATGCCTAACGCAGATGTATTT
CATGATAGCCTTGGGTAACACAGACAGCTATATTTTGGCTGCAATGGCATATGATCGAGCT
GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTCCACGGTCTTGTATCTGGC
30 TTATTGCTGGGTCTTGGGTGATTGGAAATGCCAATGCCCTCCCCACACTCTGCTCACAGC
TAGTCTGTCCTTCTGTGGCAACCAGGAAGTGGCCAACCTTCTACTGTGACATTACCCCTTG
CTGAAGTTATCCTGTTCTGACATCCACTTTCATGTGAAGATGATGTACCTAGGGGTTGGCA
TTTTCTCTGTGCCATTACTATGCATCATTGTCTCCTATATTCGAGTCTTCTCCACAGTCTTCC
AGGTTCCCTCCACCAAGGGCGTGCTCAAGGCCTTCTCCACCTGTGGTTCCACCTCACGGT
35 TGTCTCTTTGTATTATGGTACAGTCATGGGCACGTATTTCCGCCCTTGACCAATTATAGCC
TAAAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTTAAATCCTTTTCAT
CTACAGTCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAACTCTTCAACAAGAGAAT
CTCCTCGTAA (SEQ ID NO: 30)

AOLFR16 sequences:

40 MRRNCTLVTEFILLGLTSRRELQILLFTLFLAIYMTVAGNLGMIVLIQANAWLHMPMYFFLSH
LSFVDLCFSSNVTPKMLEIFLSEKKSISYPACL VQCYLFIALVHVEIYLAVMAFD RYMAICNPLL
YGSRMSKSVCSFLITVPYVYGALTGLMETMWTYNLAF CGPNEINH FYCADPPLIKLACSDTYN
KELSMFIVAGWNLSFSLFIICISYLYIFPAILKIRSTEGRQKAFSTCGSHLTAVTIFYATLFFMYLR
PPSKESVEQGMVAVFYTTVIPMLNLIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

45 ATGAGAAGAAACTGCACGTTGGTGACTGAGTTCATTCTCCTGGGACTGACCAGTCGCCGG
GAATTACAAATTCTCCTCTTACGCTGTTTCTGGCCATTTACATGGTCACGGTGGCAGGGA
ACCTTGGCATGATTGTCCTCATCCAGGCCAACGCCTGGCTCCACATGCCCATGTACTTTTC
CTGAGCCACTTATCCTTCGTGGATCTGTGCTTCTCTTCCAATGTGACTCCAAAGATGCTGG
50 AGATTTTCTTTT CAGAGAAGAAAAGCATTTTCTATCCTGCCTGTCTTGTGCACTGTTACCTT
TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGGCCTTTGACCGGTACAT
GGCCATCTGCAACCCTCTGCTTTATGGCAGCAGAATGTCCAAGAGTGTGTGCTCCTTCCTC
ATCAGGTTGCCTTATGTGTATGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA
ACCTAGCCTTCTGTGGCCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCACTGAT
55 TAAGCTGGCTTGTCTGACACCTACAACAAGGAGTTGTCAATGTTTATTGTGGCTGGCTGG
AACCTTTCTTTTCTCTCTTTCATCATATGTATTTCTACCTTTACATTTTCCCTGCTATTTTA

5 AAGATTCGCTCTACAGAGGGCAGGCCAAAAAGCTTTTTCTACCTGTGGCTCCCATCTGACAG
CTGTCACTATATTCTATGCAACCCTTTTCTTCATGTATCTCAGACCCCCCTCAAAGGAATCT
GTTGAACAGGGTAAAAATGGTAGCTGTATTTTATACCACAGTAATCCCTATGCTGAACCTTA
TAATTTATAGCCTTAGAAAATAAAAATGTAAAAGAAGCATTAATCAAAGAGCTGTCAATGA
AGATATACTTTTCTTAA (SEQ ID NO: 32)

AOLFR17 sequences:

10 MLNFTDVTEFILLGLTSRREWQVLFHIFLVVYIITMVGNI GMMVLIKVSPQLNNPMYFFLSHLS
FVDVWFSSNVTPKMLENLFSDKKTITYAGCLVQCFFFIALVHVEIFILAAMAFDRYMAIGNPLL
YGSKMSRVVCIRLITFPYIYGFLTSLAATLWTYGLYFCGKIEINH FYCADPPLIKMACAGTFVKE
YTMILAGINFTYSLTVIISYLFILAILRMRS AEGRQKAFSTCGSHLTAVIIFYGTLIFMYLRRPTE
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

15 ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGAGAAT
GGCAAGTTCTCTTCTTCATCATCTTTCTTGTGGTCTACATCATCACCATGGTGGGCAATATC
GGCATGATGGTGTTAATCAAGGTCAGTCCTCAGCTTAACAACCCCATGTACTTTTCTCTCA
GTCACCTGTCAATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAAAAC
CTGTTTTTCAGATAAAAAACAATTACTTATGCTGGTGTGTTAGTACAGTGTCTTCTTCTCAT
TGCTCTTGTCCATGTGGAAATTTTTATTCTTGTCTGCGATGGCCTTTGATAGATACATGGCAA
20 TTGGGAATCCTCTGCTTTATGGCAGTAAAATGTCAAGGGTGTCTGTATTGACTGATTAC
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT
ACTTCTGTGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGATCATACTTGCCGGCATTAACTC
ACATATCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT
25 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCCTCTGACAGCTGT
CATTATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTAA (SEQ ID NO: 34)

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AOLFR18 sequences:

MSNTNGSAITEFILLGLTDCPELQSLFLVFLVLYLVTLLGNLGMIMLMRLDSRLHTPMYFFLT
NLAFVDLCYTSNATPQMSTNIVSEKTISFAGCFTQCYIFIALLLTEFYMLAAMAYDRYVAIYDP
LRYSVKTSRRVCICLATFPYVYGFS DGLFQAILTFRLTFCRSNVINHFYCADPPLIKLSCSDTYVK
35 EHAMFISAGFNLSSLTIVLVSYAFILAAILRIKSAEGRHKAFSTCGSHMMAVTLFYGTLFCMYI
RPPTDKTVEESKIIAVFYTFVSPVLNPLIYSLRNKDV KQALKNVLR (SEQ ID NO: 35)

40 ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC
CGGAATCCAGTCTCTGCTTTTTGTGCTGTTTCTGGTGTGTTACCTCGTCACCCTGCTAGGC
AACCTGGGCATGATAATGTTAATGAGACTGGACTCTCGCCTTCACACGCCCATGTACTTCT
TCCTCACTAACTTAGCCTTTGTGGATTTGTGCTATACATCAAATGCAACCCCGCAGATGTC
GACTAATATCGTATCTGAGAAGACCATTTCTTTGCTGGTGTGTTTACACAGTGCTACATTT
TCATTGCCCTTCTACTCACTGAGTTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT
GGCCATATATGACCCTCTGCGCTACAGTGTGAAAACGTCCAGGAGAGTTTGCATCTGCTTG
45 GCCACATTTCCCTATGTCTATGGCTTCTCAGATGGACTCTTCCAGGCCATCCTGACCTTCCG
CCTGACCTTCTGTAGATCCAATGTCATCAACCACTTCTACTGTGCTGACCCGCCGCTCATTA
AGCTTTCTTGTCTGATACTTATGTCAAAGAGCATGCCATGTTTCATATCTGCTGGCTTCAAC
CTCTCCAGCTCCCTCACCATCGTCTTGGTGTCTATGCCTTCATTCTTGCTGCCATCCTCCG
GATCAAATCAGCAGAGGGAAGGCACAAGGCATTCTCCACCTGTGGTTCCTATGATGAGC
50 GTGACCCCTGTTTTATGGGACTCTCTTTTGCATGTATATAAGACCACCAACAGATAAGACT
GTTGAGGAATCTAAAATAATAGCTGTCTTTTACACCTTGTGAGTCCGGTACTTAATCCAT
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTTGAAGAATGTCCTGAGATGA
(SEQ ID NO: 36)

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AOLFR19 sequences:

METKNYSSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLTAVGNVLIILAIYSDPRLHTPMYFFLSNL
SFMDICFTTVIVPKMLVNFLSETKIISYVGLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH
YDVVMKPWHCLLMLLGSCSISHLHSLFRVLLMSRSLFCASHIHKHFFCDTQPVCLKSCSDTSSSQ
5 MVVMTETLAVIVTPFLCTIFSYLQIIVTVLRIPSAAGKWKAFTSCGSHLTVVVLFGYSVIYVYFR
PLSMYSVMKGRVATVMYTVVTPMLNPFYSLRNKDMKRGLKCLRHRIS (SEQ ID NO: 37)

ATGGAGACAAAGAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCA
ACCCTAAGCTGCAGAAACCTCTCTTTGCCATCTTCCTCATCATGTACCTACTCACTGCGGTG
10 GGAATGTGCTCATCATCTGGCCATCTACTCTGACCCCAGGCTCCACACCCCTATGTACT
TTTTTCTCAGCAACTGTCTTTTCATGGATATCTGCTTCAACAGTCATAGTGCCTAAGATG
CTGGTGAATTTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT
ACTTCTTCATGGCATTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG
GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA
15 CTCATGCTATTGGGTTCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTAT
GTCTCGCTTGCTTTCTGTGCCTCTCACATCATTAAAGCACTTTTCTGTGACACCCAGCCTG
TGCTAAAGCTCTCCTGCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTT
AGCTGTCATTGTGACCCCTTCTCTGTGTACCATCTTCTCCTACCTGCAAATCATCGTCACTG
TGCTCAGAAATCCCTCTGACGCCGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCCACCT
20 CACTGTAGTGGTCTGTTCTATGGGAGTGTCACTATGTCTATTTTAGGCCTCTGTCCATGT
ACTCAGTGATGAAGGGCCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGA
ACCTTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTTGAAGAAATTAAGAC
ACAGAATTTACTCATAG (SEQ ID NO: 38)

AOLFR20 sequences:

MVEENHTMKNEFILTGFTDHPKLTLLFVVFFAIYLLITVVGNI SLVALIFTHCR LHTPMYIFLGN
LALVDSCCACAITPKMLNFFSEGKRISLYECAVQFYFLCTVETADCFLA AVAYDRYVAICNP
LQYHIMMSKKLCIQMTTGAFIAGNLHSMIHVGLVFRLVFCGLNHINHFYCDTLPYRLSCVDPF
INELVLFIFSGSVQVFTIGSVLISYLYILLTIFRMKSKEGRAKAFSTCASHFSSVSLFYGSIFFLYIRP
30 NLLEEGGNDIPAAILFTIVVPLLNPFIYSLRNKEVISVLRKILLKIKSQGSVNK (SEQ ID NO: 39)

ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTTATCCTCACAGGATTTACAGATCACC
CTGAGCTGAAGACTCTGCTGTTTGTGGTGTCTTTGCCATCTATCTGATCACCGTGGTGGG
GAATATTAGTTTGGTGGCACTGATATTTACACACTGTCGGCTTCACACACCAATGTACATC
35 TTTCTGGGAAATCTGGCTCTTGTGGATTCTTGTGCTGTGCCTGTGCTATTACCCCCAAAATGTT
AGAGAACTTCTTTTCTGAGGGCAAAAGGATTTCCCTCTATGAATGTGCAGTACAGTTTTAT
TTTCTTTGCACTGTGGAAGTGCAGACTGCTTTCTTCTGGCAGCAGTGGCCTATGACCGCT
ATGTGGCCATCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAAACTCTGCATTCA
GATGACCACAGGCGCCTTCATAGCTGGAAATCTGCATTCCATGATTCTATGAGGGCTTGTA
40 TTTAGGTTAGTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATACTCTTCCCTT
GTATAGACTCTCCTGTGTTGACCCCTTCATCAATGAACTGGTCTATTCTCTCAGGTT
CAGTTCAAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTATATTCTTCTACTATT
TTCAGAATGAAATCCAAGGAGGGAAGGGCCAAAGCCTTTTCTACTTGTGCATCCCACCTTT
CATCAGTTTCATTATTCTATGGATCTATTTTTTCTTATACATTAGACCAAATTTGCTTGAA
45 GAAGGAGGTAATGATATACCAGCTGCTATTTTATTTACAATAGTAGTTCCTTACTAAATC
CTTTCAATTTATAGTCTGAGAAACAAGGAAGTAATAAGTGTCTTAAGAAAAATTTCTGCTGAA
AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

AOLFR21 sequences:

MEPRKNVTD FVLLGFTQNPKEQKVL FVMFLFYILTMVGNLLIVVT VTVSETLGSPMSFFLAGL
TFIDIYSSSISPR LISDLFFGNNSISFSFMAQLFIEHLFGGSEVFL LLVMA YDRYVAICKPLHYLV
IMRQWVCVLLL VVSWVGGFLQSVFQLSIYGLPFCGPNVIDHFFCDMYPLLKLA CTDTHVIGLL
VVANGGLSCTIAFL LLLISYGVLHSLKLSQKGRQKAHSTCSSHITVVVFFVPCIFMCARPAR
TFSIDKSVSVFYTVITPMLNPLIYTLRNSEMTSAMKKL (SEQ ID NO: 41)

ATGGAGCCAAGGAAAAATGTGACTGACTTTGTCCTCTTGGGCTTCACACAGAATCCAAAG
GAGCAGAAAGTACTTTTTGTTATGTTCTTGCTCTTCTACATTTTGACCATGGTGGGCAACCT
GCTCATTGTAGTGACCGTAACTGTCAGTGAGACCCTGGGCTCACCAATGTCCTTCTTTCTT
GCTGGCTTAACATTTATAGATATCATTATTTCTTCATCCATTTCCCCCAGATTGATTTCAGA
5 CTTGTTCTTTGGGAATAATTCCATATCCTTCCAATCTTTCATGGCCCAGCTCTTTATCGAGC
ACCTTTTTTGGTGGGTGAGAGGTCTTCTCCTGTTGGTGATGGCCTATGACCGCTATGTGGC
CATCTGTAAGCCCTTGCATTATTTGGTTATCATGAGACAATGGGTGTGTGTTTTGCTGCTG
GTAGTGTCTGGGTTGGAGGATTTCTGCAATCAGTATTTCAACTTAGCATTATTTATGGGC
TCCCATTCTGTGGCCCCAATGTCATTGATCATTTTTTCTGTGACATGTATCCCTTATTGAAA
10 CTGGCCTGCACTGACACCCATGTTATTTGGCCTCTTAGTGGTGGCCAATGGAGGACTGTCTT
GCATATTGCGTTTTCTGCTCTTACTCATCTCTTATGGTGTGCATCCTGCACCTCTCTAAAGAAA
CTTAGTCAGAAAGGGAGGCAAAAAGCCCCACTCAACCTGCAGTTCCACATCACTGTGGTTG
TCTTCTTCTTTGTTCTTGTATTTTTATGTGTGCTAGACCTGCTAGGACCTTCTCCATTGAC
AAATCAGTGAGTGTGTTTTATACAGTCATAACCCCAATGCTGAACCCCTTAATCTACACTC
15 TGAGAAATTCTGAGATGACAAGTGCTATGAAGAAGCTTTAG (SEQ ID NO: 42)

AOLFR22 sequences:

MRXXNXXTEFVLLGFSQDPGVXKALFVMFLLYXXTVVGNLLIVVDIIASPLXGSPMYFFLAC
LSFIDAAYSTTISPKLIVGLFCDKKTISFQCGMGQLFIDHFFGGAEVLLVVMACDRYVAICKPL
20 HYLTIMNRQVCFLLLVXXMIGGFVHSAFQIVVYSLPFCGPXVIVHFSCDMHPLLELACTDTYFI
GLTVVNSGAICMVIFNLLISYGVILSSLKTYSQEKRGKALSTCSSGSTVVVLFVPCIFYVRP
VSNFPTDKFMTVFYTIITHMLSPLIYTLRNSEMRNAIEKLLGKKLTIFIIGGVSVLM (SEQ ID NO:
43)

ATGAGACANNNNAACAATATNACAGAATTTGTCCTCCTGGGCTTTTCTCAGGATCCTGGTG
TGNNNAAAGCATTATTTGTCATGTTTTACTCACATAACNNNNNACAGTGGTGGGGAACCT
GCTCATTGTNGTGGATATTATTGCCAGCCCTTNNTTGGGTTCCCCAATGTATTTCTTCCTTG
CCTGCCTGTCATTTATAGATGCTGCATATTCCTACTACCATTTCTCCCAAGTTAATTGTAGGC
TTATTCTGTGATAAAAAGACTATTTCTTCCAAGGTTGCATGGGCCAGCTATTTATAGACC
30 ATTTCTTTGGTGGGGCTGAGGTCTTCTTCTGGTGGTGATGGCCTGTGATCGCTATGTGGC
CATCTGTAAGCCACTGCACTATTTGACCATCATGAATCGACAGGTTTGCTTCTTCTGTTGG
TNNTNNCCATGATTGGAGGTTTTGTACATTCTGCGTTTCAAATTGTTGTGTACAGTCTCCCT
TTCTGTGGTCCCNAATGTCATTGTTTCATTTCAGTTGTGACATGCACCCATTACTGGAAGTGGC
ATGCACTGACACCTACTTTATAGGCCTCACTGTTGTGTGCAATAGTGAGCAATCTGTATG
35 GTCATTTTCAACCTTCTGTTAATCTCCTATGGAGTCATCCTAAGCTCCCTTAAACCTTACAG
TCAGGAAAAGAGGGGTAAAGCCTTGTCTACCTGCAGCTCCGGCAGTACCGTTGTTGTCCTC
TTTTTTGTACCCTGTATTTTCATATATGTTAGACCTGTTTCAAACCTTCTCTACTGATAAGTT
CATGACTGTGTTTTATACCATTATCACACACATGCTGAGTCCTTTAATATATACGTTGAGA
AATTCAGAGATGAGAAATGCTATAGAAAACTCTTGGGTAAAAAGTTAACTATATTTATTA
40 TAGGAGGAGTGTCCGTCCTCATGTAG (SEQ ID NO: 44)

AOLFR23 sequences:

MAKNNLTRVTEFILMGFMDHPKLEIPLFLVFLSFYLVTLGNVGMIMLIQVDVKLYTPMYFFLS
HLSLLDACYTSVITPQILATLATGKTVISYGHCAAQFFLTICAGTECFLLAVMAYDRYAAIRNP
45 LLYTVAMNPRLCWLSLVGAYVCGVSGAILRTTCTFTLSFCKDNQINFFCDLPLLLKLACSDTA
NIEIVIFFGNFVILANASVILISYLLIKTILKVKSSGGRKTFSTCASHITAVALLFFGALIFMYLQS
GSGKSLEEDKVVSFVYTVVIPMLNPLIYSLRNKDVKDAFRKVARRLQVSLSM (SEQ ID NO: 45)

ATGGCCAAGAATAATCTCACCAGAGTAACCGAATTCATTCTCATGGGCTTTATGGACCACC
50 CCAAATTGGAGATTCCCCTCTTTCTGGTGTTTCTGAGTTTCTACCTAGTCACCCTTCTTGGG
AATGTGGGGATGATTATGTAAATCCAAGTAGATGTCAAACCTCTACACCCCAATGTACTTCT
TCCTGAGCCACCTCTCCCTGCTGGATGCCTGTTACACCTCAGTCATCACCCCTCAGATCCTA
GCCACATTGGCCACAGGCAAAACGGTCATCTCCTACGGCCACTGTGCTGCCAGTTCTTTT
TATTCACCATCTGTGCAGGCACAGAGTGCTTTCTGCTGGCAGTGATGGCCTATGATCGCTA
55 TGCTGCCATTGCAACCCACTGCTCTATACCGTGGCCATGAATCCCAGGCTCTGCTGGAGC
CTGGTGGTAGGAGCCTATGTCTGTGGGGTGTGAGGAGCCATCCTGCGTACCCTTGACCT

TCACCTCTCCTTCTGTAAGGACAATCAAATAAACTTCTTCTTCTGTGACCTCCCACCCCTG
CTGAAGCTTGCCTGCAGTGACACAGCAAACATCGAGATTGTCATCATCTTCTTTGGCAATT
TTGTGATTTTGGCCAAATGCCTCCGTATCCTGATTTCTATCTGCTCATCATCAAGACCATT
TTGAAAGTGAAGTCTTCAGGTGGCAGGGCCAAGACTTTCTCCACATGTGCCTCTCACATCA
5 CTGCTGTGGCCCTTTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAAGTGGCTCAGGCAAA
TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCATCCCCATGCTGAACC
CTCTGATCTACAGCTTAAGAAACAAAGATGTAAAAGACGCCTTCAGAAAGGTCGCTAGGA
GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

10 **AOLFR25 sequences:**

METGNLTWVSDFVFLGLSQTRELQRFLFLMFLFVYITTVMGNILIITVTSDSLHTPMYFLLRN
LAVLDLCFSSVTAPKMLVDLLSEKKTISYQCGMGQIFFFHFLGGAMVFFLSVMAFDRLIAISRPL
RYVTVMNTQLWVGLVVA TWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVRLACTDT
SLLEFLKISNSGLLDVWVFFLLMSYLFILVMLRSHPGARRKAASTCTTHIIVVSMIFVPSIYLY
15 ARPFTFPMDKLVSIGHTVMTPLNPMIYTLRNQDMQAAVRRLGRHRLV (SEQ ID NO: 47)

ATGGAAACAGGGAACCTCACGTGGGTATCAGACTTTGTCTTCCTGGGGCTCTCGCAGACTC
GGGAGCTCCAGCGTTTCTGTTTCTAATGTTTCTGTTTGTCTACATCACCCTGTTATGGGA
AACATCCTTATCATCATCAGTGACCTCTGATTCCAGCTCCACACACCCATGTACTTTCT
20 GCTCCGAAACCTGGCTGTCTAGACCTCTGTTTCTCTTCAGTCACTGCTCCAAAATGCTAG
TGGACCTCCTCTCTGAGAAGAAAACCATCTCTTACCAGGGCTGCATGGGTGAGATCTTCTT
CTTCCACTTTTTTGGGAGGTGCCATGGTCTTCTTCTCTCAGTGATGGCCTTTGACCGCCTCA
TTGCCATCTCCCGGCCCTCCGCTATGTCACCGTCATGAACACTCAGCTCTGGGTGGGGCT
GGTGGTAGCCACCTGGGTGGGAGGCTTTGTCCACTCTATTGTCCAGCTGGCTCTGATGCTC
25 CCACTGCCCTTCTGTGGCCCAACATTTTGGATAACTTCTACTGTGATGTTCCCAAGTACT
GAGACTTGCTGCACTGACACCTCACTGCTGGAGTTCCTCAAGATCTCCAACAGTGGGCTG
CTGGATGTCGTCTGGTCTTCTCTCTCTGATGTCCTACTTATTCATCCTGGTGATGCTGAG
GTCACATCCAGGGGAGGCAAGAAGGAAGGCAGCTTCCACCTGCACCACCCACATCATCGT
GGTTTCCATGATCTTCGTTCCAAGCATTTACCTCTATGCCCGGCCCTTCACTCCATTCCCTA
30 TGGACAAGCTTGTGTCCATCGGCCACACAGTCATGACCCCATGCTCAACCCCATGATCTA
TACCCTGAGGAACCAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT
TTGA (SEQ ID NO: 48)

AOLFR26 sequences:

MAAKNSSVTEFILEGLTHQPGLRIPLFFLFLGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLFNLS
LIDFCFSTTTITPKMLMSFVSRKNISFTGCMTQLFFFCFFVVSSEFILSAMAYDRYVAICNPPLYT
VTMSCQVCLLLL GAYGMGFAGAMAHTGSIMNLTFCADNLVNHFMCDILPILLESCNSSYMN
BLVVFIVVAVDVGMPIVTVFISYALILSSILHNSSTEGRSKAFSTCSSHIVVSLFFGSGAFMYLKP
LSILPLEQGVSSLFYTIIVPVLNPLIYSLRNKDVKVALRRTLGRKIFS (SEQ ID NO: 49)

40 ATGGCAGCCAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGG
GACTGCGGATCCCCCTCTTCTTCTGTTTCTGGGTTTCTACACGGTCACCGTGGTGGGGAA
CCTGGGCTTGATAACCCTGATTGGGCTGAACTCTCACCTGCACACTCCCATGTACTTCTTCC
TTTTAACCTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAAATGCTGATG
45 AGTTTTGTCTCAAGGAAGAACATATTTCTTTCACAGGGTGTATGACTCAGCTCTTCTTCTT
CTGCTTCTTTGTCTCTCTGAGTCCTTCATCCTGTCAGCGATGGCGTATGACCGCTACGTGG
CCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTGCTCCTTTTG
TTGGGTGCCTATGGGATGGGGTTTGCTGGGGCCATGGCCACACAGGAAGCATAATGAAC
CTGACCTTCTGTGCTGACAACCTTGTCATCATTTTCATGTGTGACATCCTTCTCTCCTTGA
50 GCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTGGTGGCTGTTGAC
GTTGGAATGCCCATTTGTCAGTGTCTTTATTTCTTATGCCCTCATCCTCTCCAGCATCTACA
CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCAGTTCCACATAATTGTA

AOLFR27 sequences:

MPSQNYSIIEFNLFGFSAFPQHLLPILFLLYLLMFLFTLLGNLLIMATIWIHRLHTPMYFLCTL
 SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFGFTHSFLLLVMGYDRYVAICHPLR
 5 YNVLMSPRDCAHLVACTWAGGSVMGMMVTTIVFHLTFCGSNVIHHFFCHVLSLLKLACENKT
 SSVIMGVMLVCVTALIGCLFLIILSYVFIVAAILRIPSAEGRHKTFSTCVSHLTVVVTHYSFASFIY
 LKPKGLHSMYSDALMATTYTVFTPFLSPIIFSLRNKELKNAINKNFYRKFCPPSS (SEQ ID NO:
 51)

10 ATGCCTAGTCAGAACTATAGCATCATATCTGAATTTAACCTCTTTGGCTTCTCAGCCTTCCC
 CCAGCACCTCCTGCCCATCTTGTTCTGCTGTACCTCCTGATGTTCTGTTACATTGCTGG
 GCAACCTTCTCATCATGGCCACAATCTGGATTGAACACAGACTCCACACACCCCATGTACCT
 CTTCTTGTGCACCCTCTCCGCTCTCTGAGATTCTGTTCACTGTTGCCATCACCCCTCGCATGC
 TGGCTGATCTGCTTTCCACCCATCATTCATCACCTTTGTGGCTTGTGCCAACAGATGTTCT
 15 TTCTCCTTCATGTTTGGCTTCACTCACTCCTTCTCCTTCTCCTGGTCATGGGCTATGATCGCTA
 TGTGGCCATCTGCCACCCACTGCGTTACAATGTGCTCATGAGCCCCCGTGACTGTGCCAT
 CTTGTGGCCTGTACCTGGGCTGGTGGCTCAGTCATGGGGATGATGGTGACAACGATAGTTT
 TCCACCTCACTTTCTGTGGGTCTAATGTGATCCACCATTTTTTCTGTCATGTGCTTTCCCTCT
 TGAAGTTGGCCTGTGAAAAACAAGACATCATCTGTCATCATGGGTGTGATGCTGGTGTGTGT
 20 CACAGCCCTGATAGGCTGTTTATTCCTCATCATCCTCTCCTATGTCTTCATTGTGGCTGCCA
 TCTTGAGGATTCCCTCTGCCGAAGGCCGGCACAAGACATTTTCTACGTGTGTATCCCACCT
 CACTGTGGTGGTCACGCACTATAGTTTTCCTCCTTTATCTACCTCAAGCCCAAGGGCCTCC
 ATTCTATGTACAGTGACGCCTTGATGGCCACCACCTATACTGTCTTCACCCCTTCCTTAGC
 CCAATCATTTTTCAGCCTAAGGAACAAGGAGCTGAAGAATGCCATAAATAAAAACTTTTACA
 25 GAAATTCTGTCTCCAAGTTCCTGA (SEQ ID NO: 52)

AOLFR28 sequences:

MPNFTDVTEFTLLGLTCRQELQVLFFVFLAVYMITLLGNIGMIILISISPQLQSPMYFFLSHLSF
 ADVCFSSNVTPKMLENLLSETKTISYVGCLVQCYFFIAVVHVEVYILAVMAFDYRMAGCXPLL
 30 YGSKMSRTVCVRLISVXYXYGFSVSLICTLWTYGLYFCGNFEINHFYCADPPLIQIACGRVHIKE
 ITMIVIAGINFYISLSVVLISYTLIVVAVLRMRSADGRRKAFSTCGSHLTAVSMFYGTPIFMYLR
 RPTEESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKEAVNKAITKTYVRQ (SEQ ID NO: 53)

35 ATGCCTAATTTACGGATGTGACAGAATTTACTCTCCTGGGGCTGACCTGTCGTCAGGAGC
 TACAGGTTCTCTTTTTTGTGGTGTTCCTAGCGGTTTACATGATCACTCTGTTGGGAAATATT
 GGTATGATCATTTTGATTAGCATCAGTCTCCTCAGCTTACAGAGTCCCATGTACTTTTCTGAG
 TCATCTGCTTTTGGCGACGTGTGCTTCTCCTCCAACGTTACCCCCAAAATCTGGAAAACT
 TATTATCAGAGACAAAAACCATTTCCTATGTGGGATGCTTGGTGCAGTGCTACTTTTTCAT
 TGCCGTTGTCCACGTGGAGGTCTATATCCTGGCTGTGATGGCCTTTGACAGGTACATGGCC
 40 GGCTGCAANCCTCTGCTTTATGGCAGTAAAATGTCTAGGACTGTGTGTGTTCGGCTCATCT
 CTGTGNNNTATGNNNTATGGATTCTCTGTGACGCTAATATGCACACTATGGACTTATGGCTT
 ATACTTCTGTGGAACTTTGAAATCAATCACTTCTATTGTGCAGATCCCCCTCTCATCCAGA
 TTGCCTGTGGGAGAGTGCACATCAAAGAAATCACAATGATTGTTATTGCTGGAATTAACCT
 CACATATCCCTCTCGGTGGTCTCATCTCCTACACTCTCATTGTAGTAGCTGTGCTACGCA
 45 TGCGCTCTGCCGATGGCAGGAGGAAGGCGTTCTCCACCTGTGGGTCCCACTTGACGGCTGT
 TTCTATGTTTTATGGGACCCCCATCTTCATGTATCTCAGGAGACCCACTGAGGAATCCGTA
 GAGCAGGGCAAAATGGTGGCTGTGTTTTACACCACAGTAATTCTATGTTGAATCCCATGA
 TCTACAGTCTGAGAAATAAGGATGTAAAAGAAGCAGTCAACAAAGCAATCACCAAGACAT
 ATGTGAGGCAGTAA (SEQ ID NO: 54)

50

AOLFR29 sequences:

MMSFAPNASHSPVFLLLGFSRANISYTLFFFLFLAIYLTTLGNVTLVLLISWDSRLHSPMYYYLLR
 GLSVIDMGLSTVTLPLQLLAHLVSHYPTIPAARCLAQFFFFYAFGVTDTLVIAVMALDRYVAICD
 PLHYALVMNHQRACLLALSWVVSILHTMLRVGLVPLCWTGDAGGNVNLPHFFCDHRPLLR
 55 ASCSDIHSNELAIFFEFGFLMLGPCALIVLSYVRIGAAAILRLPSAAGRRAVSTCGSHLTMVGFL

YGTIHCVYFQPPFQNSQYQDMVASVMYTAITPLANPFVYSLHNKDVKGALCRLLEWVKVDP
(SEQ ID NO: 55)

5 ATGATGAGCTTTGCCCTAATGCTTCACACTCTCCGGTTTTTTTGCTCCTTGGGTCTCGAG
AGCTAACATCTCCTACACTCTCCTCTTCTCCTGTTCTGCTATTTACCTGACCACCATAC
TGGGGAATGTGACACTGGTGCTCATCTCCTGGGACTCCAGACTGCACTCACCCATGTA
TTATCTGCTTCGTGGCCTCTCTGTGATAGACATGGGGCTATCCACAGTTACACTGCCCCAG
TTGCTGGCCCATTTGGTCTCTCATTACCCAACCATTCTGCTGCCCCGCTGCTTGGCTCAGTT
CTTTTTCTTCTATGCATTTGGGGTTACAGATACACTTGTCAATTGCTGTGCTGCTGCTGATC
10 GCTATGTGGCCATCTGTGACCCCCTGCACTATGCTTTGGTAATGAATCACCAACGGTGTGC
CTGCTTACTAGCCTTGAGCTGGGTGGTGTCCATACTGCACACCATGTTGCGTGTGGGACTC
GTCCTGCCTCTTTGCTGGACTGGGGATGCTGGGGGCAACGTTAACCTTCTCACTTCTTTTG
TGACCACCGGCCACTTCTGCGAGCCTCTTGTCTGACATACATTCTAATGAGCTGGCCATA
TTCTTTGAGGGTGGCTTCCTTATGCTGGGGCCCTGTGCCCTCATTGTACTCTCTTATGTCCG
15 AATTGGGGCCGCTATTCTACGTTTGCCTTCAGCTGCTGGTGCAGCCGCGAGCAGTCTCCACC
TGTGGATCCACCTCACCATGGTTGGTTTCCTCTACGGCACCATCATTTGTGTCTACTTCCA
GCCTCCCTTCCAGAACTCTCAGTATCAGGACATGGTGGCTTCAGTAATGTATACTGCCATT
ACACCTTTGGCCAACCCATTTGTGTATAGCCTCCACAATAAGGATGTCAAGGGTGCCTCT
GCAGGCTGCTTGAATGGGTGAAGGTAGACCCCTGA (SEQ ID NO: 56)

20 **AOLFR30 sequences:**
MGFLSPMHPCRPPTQRRMAAGNHSTVTEFILKGLTKRADLQLPLFLLFLGIYLVTVGNLGMIT
LICLNSQLHTPMYFSLNLSMDLCYSSVITPKMLVNFVSEKNIISYAGCMSQLYFFLVFVIAEC
YMLTVMAYDRYVXXCHPLLNIIMSHHTCLLVAVVYAIGLIGSTIETGLMLKLPYCEHLISHY
25 FCDILPLMKLSCSSTYDVENTVFFSAGFNHIVTSLTVLSYTFILSSILGISTTEGRSKAFSTCSSHL
AAVGMFYGSTAFMYLKPSTISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKA AVQKTLRGK
LF (SEQ ID NO: 57)

30 ATGGGGTTCTTGTCTCCCATGCATCCCTGCAGGCCTCCCACCCAGAGGAGAATGGCTGCAG
GAAATCACTCTACAGTGACAGAGTTTATTCTCAAGGGTTTAACGAAGAGAGCAGACCTCC
AGTCCCCCTCTTTCTCCTCTCCTCGGGATCTACTTGGTCACCATCGTGGGGAACCTGGGC
ATGATCACTCTAATTTGTCTGAACTCTCAGCTGCACACCCCATGTACTACTTTCTCAGCAA
TCTGTCACTCATGGATCTCTGCTACTCCTCCGTCATTACCCCTAAGATGCTGGTGAACTTTG
35 TGTCAGAGAAAAACATCATCTCCTACGCAGGGTGCATGTCACAGCTCTACTTCTTCTTGT
TTTTGTCATTGCTGAGTGTTACATGCTGACAGTGATGGCCTACGACCGCTATGTTGNCNTC
TGCCACCCTTTGCTTTACAACATCATTATGTCTCATCACACCTGCCTGCTGCTGGTGGCTGT
GGTCTACGCCATCGGACTCATTGGCTCCACAATAGAACTGGCCTCATGTTAAACTGCCC
TATTGTGAGCACCTCATCAGTCACTACTTCTGTGACATCCTCCCTCTCATGAAGCTGTCTGT
CTCTAGCACCTATGATGTTGAGATGACAGTCTTCTTTTCGGCTGGATTCAACATCATAGTC
40 ACGAGCTTAACAGTTCTTGTCTTACACCTTCATTCTCTCCAGCATCCTCGGCATCAGCAC
CACAGAGGGGAGATCCAAAGCCTTCAGCACCTGCAGCTCCCACCTTGCAGCCGTGGGAAT
GTTCTATGGATCAACTGCATTATGTACTTAAACCCCTCCACAATCAGTTCCTTGACCCAG
GAGAATGTGGCCTCTGTGTTCTACACCACGGTAATCCCCATGTTGAATCCCCTAATCTACA
GCCTGAGGAACAAGGAAGTAAAGGCTGCCGTGCAGAAAACGCTGAGGGGTAAACTGTTTT
45 GA (SEQ ID NO: 58)

AOLFR31 sequences:
MGTGNDTTVVEFTLLGLSEDTTVCAILFLVFLGIYVVTLMGNISIIVLIRRSHHLHTPMYIFLCHL
AFVDIGYSSSVTPVMLMSFLRKETSLPVAGCVAQLCSVVTFGTAECFLAAMAYDRYVAICSP
50 LLYSTCMSPGVCILVGMSYLGCVNAWTFIGCLRLSFCGPNKVNHHFCDSPLKLACSHDF
TFEII PAISSGSIVATVCVIAISYIYLITILKMHSTKGRHKAFSTCTSHLTAVTLFYGTTTFIYVMP
KSSYSTDQNKVVS VFYTVVIPMLNPLIYSLRNKEIKGALKRELRIKIFS (SEQ ID NO: 59)

55 ATGGGGACTGGAAATGACACCACTGTGGTAGAGTTTACTCTTTTGGGGTTATCTGAGGATA
CTACAGTTTGTGCTATTTTATTTCTTGTGTTTCTAGGAATTTATGTTGTACCTTAATGGGT
AATATCAGCATAATTGTATTGATCAGAAGAAGTCATCATCTTCATACACCCATGTACATT

TCCTCTGCCATTTGGCCTTTGTAGACATTGGGTACTCCTCATCAGTCACACCTGTCATGCTC
ATGAGCTTCCTAAGGAAAGAAACCTCTCTCCCTGTTGCTGGTTGTGTGGCCCAGCTCTGTT
CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCTGCTGGCTGCCATGGCCTATGATCGCTA
TGTGGCCATCTGCTCACCCCTGCTCTACTCTACCTGCATGTCCCCTGGAGTCTGCATCATCT
5 TAGTGGGCATGTCTACCTGGGTGGATGTGTGAATGCTTGGACATTCAATTGGCTGCTTATT
AAGACTGTCCTTCTGTGGGCCAAATAAAGTCAATCACTTTTTCTGTGACTATTCACCACTTT
TGAAGCTTGCTTGTTCCTATGATTTTACTTTTGAATAAATCCAGCTATCTCTTCTGGATCT
ATCATTGTGGCCACTGTGTGTGCATAGCCATATCCTACATCTATATCCTCATCACCATCCT
10 GAAGATGCATCCACCAAGGGCCGCCACAAGGCCTTCTCCACCTGCACCTCCCACCTCACT
GCAGTCACTCTGTTCTATGGGACCATTACCTTCATTTATGTGATGCCCAAGTCCAGCTACTC
AACTGACCAGAACAAGGTGGTGTCTGTGTTCTACACCGTGGTGATTCCCATGTTGAACCCC
CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA
AAAATATTTTCTTGA (SEQ ID NO: 60)

15 AOLFR32 sequences:

MNSLKDGNHTALTGFILLGLTDDPILRVILFMIILSGNLSIILIRISSQLHHPMYFFLSHLAFADM
AYSSSVTPNMLVNFLVERNTVSYLGCAIQLGSAFFATVECVLLAAMAYDRFVAICSPLLYSTK
MSTQVSVQLLL VVYIAGFLIAVSYTTSFYFLLFCGPNQVNHFFCDFAPLLELSCSDISVSTVVLFS
SSGSIIIVTVCVIAVCYIYLITILKMRSTEGHHKAFSTCTSHLTVVTLFYGTITFIYVMPNFSYST
20 DQNKVVSVLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNDIT (SEQ ID
NO: 61)

ATGAATTCCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA
CAGATGATCCAATCCTTCGAGTCATCCTCTTCATGATCATCCTATCTGGTAATCTCAGCATA
25 ATTATTCTTATCAGAATTTCTTCTCAGCTCCATCATCCTATGTATTTCTTTCTGAGCCACTT
GGCTTTTGCTGACATGGCCTATTCATCTTCTGTACACCCCAACATGCTTGTAACCTTCCTGG
TGGAGAGAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTCAGCGGCTTTCTT
TGCAACAGTGAATGCGTCCTTCTGGCTGCCATGGCCTATGACCGCTTTGTGGCAATTTGC
AGTCCACTGCTTTATTCAACCAAAAATGTCCACACAAGTCAGTGTCCAGCTACTCTTAGTAG
30 TTTACATAGCTGGTTTTCTCATTGCTGTCTCCTATACTACTTCCTTCTATTTTTTACTCTTCT
GTGGACCAAAATCAAGTCAATCATTTTTTCTGTGATTTTCGCTCCCTTACTTGAACCTCCTGT
TCTGATATCAGTGTCTCCACAGTTGTTCTCTCATTTTTCTTCTGGATCCATCATTGTGGTCAC
TGTGTGTGTGCATAGCCGTCTGCTACATCTATATCCTCATCACCATCCTGAAGATGCGCTCCA
CTGAGGGGGCACCACAAGGCCTTCTCCACCTGCACCTCCCACCTCACTGTGGTTACCCTGTT
35 CTATGGGACCATTACCTTCATTTATGTGATGCCCAATTTAGCTACTCAACTGACCAGAAC
AAGGTGGTGTCTGTGTTGTACACAGTGGTGATTCCCATGTTGAACCCCTGATCTACAGCC
TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTTAGAAAAATACTTTCTC
ATGATGCTTGTTATTTTAGTAGAACTTCAAATAATGATATTACATAG (SEQ ID NO: 62)

40 AOLFR34 sequences:

MLEGVEHLLLLLLLDVNSKELQSGNQTSVSHFILVGLHHPQLGAPLFLAFLVIYLLTVSGNG
LIILTVLVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLGSRIISFGGCVIQLFSFHLGCT
ECFLYTLMA YDRFLAICKPLHYATIMTHRVCNSLALGTWLGGTIHSFLQTSFVRLPFCGPNRV
DYIFCDIPAMRLACADTAINELVTFADIGFLALTCFMLILTSYGYIVAAILRIPSADGRNFAST
45 CAAHLTVVIVYYVPCTFIYLRPCSQEPLDGVVAVFYTVITPLLSIIYTLCNKEMKAALQRLGG
HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTTGAGCATCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG
AACTGCAAAGTGGAACCAAGACTTCTGTGTCTCACTTCATTTGGTGGGCTGCACCAACC
50 ACCACAGCTGGGAGCGCCACTCTTCTTAGCTTTCCTTGTCACTATCTCCTCACTGTTTCTG
GAAATGGGCTCATCATCCTCACTGTCTTAGTGGACATCCGGCTCCATCGTCCCAGTGTGCTT
GTTCTGTGTCACTCTCCTTCTTGGACATGACCATTCTTGTGCTATTGTCCCCAAGATGC
TGGCTGGCTTTCTTCTGGGTAGTAGGATTATCTCCTTTGGGGGCTGTGTAATCCAACATTT
TCTTTCCATTTCTGGGCTGTACTGAGTGCTTCTTTACACACTCATGGCTTATGACCGTTT
55 CCTTGCCATTTGTAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCTGTAACCTCCC
TGGCTTTAGGCACCTGGCTGGGAGGGACTATCCATTCACTTTTCCAAACAAGTTTTGTATT

TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCCCTTAG
(SEQ ID NO: 68)

AOLFR37 sequences:

5 MEKANETSPVMGFVLLRLSAHPELEKTFVLLMYLVILLGNGVLILVTILDSRLHTPMYFFLG
NLSFLDICFTTSSVPLVLDSTLTPQETISFSACAVQMALSFAMAGTECLLSMMAFDYVAICNP
LRYSVIMSKAAYMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS
INVISMEVTNVIFLGVPVLFISFSYVFIITILRIPSAEGRKKVFSTCSAHLTVVIVFYGTLFFMYG
10 KPKSKDSMGADKEDLSDKLIPLFYGVVTPMLNPIIYSLRNKDVKAAVRRLLRPKGFTQ (SEQ ID
NO: 69)

ATGGAAAAAGCCAATGAGACCTCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCCC
ACCCAGAGCTGGAAAAGACATTCTTCGTGCTCATCCTGCTGATGTACCTCGTGATCCTGCT
GGGCAATGGGGTCTCATCCTGGTGACCATCCTGACTCCCGCCTGCACACGCCCATGTAC
15 TTCTTCTAGGGAACCTCTCCTTCTGGACATCTGCTTCACTACCTCCTCAGTCCCCTGGT
CCTGGACAGCTTTTTGACTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG
GCACTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTGATC
GCTATGTGGCCATCTGCAACCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCCTACAT
GCCCATGGCTGCCAGCTCCTGGGCTATTGGTGGTGCTGCTTCCGTGGTACACACATCCTTG
20 GCAATTCAGCTGCCCTTCTGTGGAGACAATGTCATCAACCACTTCACCTGTGAGATTCTGG
CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA
TGTGATCTTCTAGGAGTCCCGTTCTGTTCATCTCTTCTCCTATGTCTTCATCATCACC
CCATCCTGAGGATCCCTCAGCTGAGGGGAGGAAAAAGGTCTTCTCCACCTGCTCTGCCCA
CCTCACCGTGGTGATCGTCTTCTACGGGACCTTATTCTTCATGTATGGGAAGCCTAAGTCT
25 AAGGATCCATGGGAGCAGACAAAGAGGATCTTTCAGACAAATCATCCCCCTTTCTATG
GGTGGTGACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG
CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)

AOLFR38 sequences:

30 MYLVTVLRNLLILAVSSDSLHTPMCFFLSNLCWADIGFTSAMVPMIVDMQSHSRVISYAGC
LTQMSFFVLFACIEDMLLTVMAYDRFVAICHPLHYPVIMNPHLGVLVLVSFFLSLLDSQLHSW
IVLQFTFFKNVEISNFVCDPSQLNLACSDSVINSIFIYLDSIMFGFLPISGILLSYANNVPSILRISS
SDRKSFASTCGSHLAVVCLFYGTGIGVYLTSAVSPPPRNGVVASVMYAVVTPMLNPFIIYSLR
NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)

35 ATGTACCTGGTCACGGTGCTGAGGAACCTGCTCATCATCCTGGCTGTCAGCTCTGACTCCC
ACCTCCACACCCCCATGTGCTTCTTCTCTCCAACCTGTGCTGGGCTGACATCGGTTTACC
TCGGCCATGGTTCCCAAGATGATTGTGGACATGCAGTCGCATAGCAGAGTCATCTCTTATG
CGGGCTGCCTGACACAGATGTCTTTCTTTGTCTTTTTCATGTATAGAAGACATGCTCCTG
40 ACAGTGATGGCCTATGACCGATTTGTGGCCATCTGTCACCCCTGCACTACCCAGTCATCA
TGAATCCTCACCTTGGTGTCTTCTTAGTTTTGGTGTCTTTTCTCCTCAGCCTGTTGGATTCC
CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAAATCTCCAATT
TTGTCTGTGACCCATCTCAACTTCTCAACCTTGCTGTCTGACAGTGTCATCAATAGCATA
TTCATATATTTAGATAGTATTATGTTTGGTTTTCTTCCCATTTCAAGGATCCTTTTGTCTTAC
45 GCTAACAAATGTCCCTCCATTCTAAGAATTTTCATCATCAGATAGGAAGTCTAAAGCCTTCT
CCACCTGTGGCTCTCACCTGGCAGTTGTTTGTCTATTTTATGGAACAGGCATTGGCGTGTA
CCTGACTTCAGCTGTGTCAACACCCCCAGGAATGGTGTGGTGGCATCAGTGATGTACGCT
GTGGTCACCCCATGCTGAACCCCTTTCATCTACAGCCTGAGAAATAGGGACATTCAAAGTG
CCCTGTGGAGGCTGCGCAGCAGACGAATCTCATGATCTGTTATCTCAAGATCTGCT
50 CCATCCTTTTTCTTGTGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)

AOLFR39 sequences:

MGVKNHSTVTEFLLSGLTEQAEQLPLFLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS
LSFLDFCYSSVITPKMLSGFLCRDRSISYSGCMIQLFFFCVVCVISECYMLAAMACDRYVAICSP
55 LYRVIMSPRVCSLLVAAVFSVGFTDAVIHGGCILRLSFCGSNIIKHVFCDIVPLIKLSCSSTYIDEL

5 TTCCTGCGGAATTTCTCCTTCCTGGAGCTGTTGCTGGTAACTGTTGTGGTTCCCAAGATGCT
 TGTCGTCATCCTCACGGGGGATCACACCATCTCATTTGTCAGCTGCATCATCCAGTCCTACC
 TCTACTTCTTTCTAGGCACCACTGACTTCTTCCTCTTGGCCGTCATGTCTCTGGATCGTTAC
 CTGGCAATCTGCCGACCACTCCGCTATGAGACCCTGATGAATGGCCATGTCTGTTCCCAAC
 10 TAGTGCTGGCCTCCTGGCTAGCTGGATTCTCTGGGTCTTTGCCCCACTGTCCTCATGGCC
 AGCCTGCCTTTCTGTGGCCCCAATGGTATTGACCACTTCTTTCGTGACAGTTGGCCCTTGCT
 CAGGCTTTCTTGTGGGGACACCCACCTGCTGAACTGGTGGCTTTCATGCTCTCTACGTTG
 GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCCTATGCCTGCATTCTTGCCACTGTTCT
 CAGGGCCCCCTACAGCTGCTGAGCGAAGGAAAGCGTTTTTCCACTTGCCTCGCATCTTACA
 15 GTGGTGGTCATCATCTATGGCAGTTCATCTTTCTCTACATTCGTATGTCAGAGGCTCAGTC
 CAAACTGCTCAACAAAGGTGCCTCCGTCCTGAGCTGCATCATCACACCCCTCTTGAACCCA
 TTCATCTTCACTCTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTTGGGGTGGC
 CCAGGCTCACTGCTGTGATGAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO:
 78)

AOLFR42 sequences:

15 MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSAVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL
 GNLSFLDFCYSSITAPRMLVDLLSGNPTISFGGCLTQLFFHFHIGGIKIFLLTVMAYDRYIAISQPL
 20 HYTLIMNQTVCALLMAASVWVGFIHSIVQIALTIQLPFCGPDKLDNFYCDVPQLIKLACTDTFV
 LELLMVSNGLVTLMLCFLVLLGSYTALLVMLRSHSREGRSKALSTCASHIAVVTLIFVPCIYVY
 TRPFRTPMDKAVSVLYTIVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGPLEHRPLH
 (SEQ ID NO: 79)

25 ATGAATCCAGCAAATCATTCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT
 GGGAGCTTCGGTTTGTCTTCTTCTACTGTTTCTCTGCTGTGTATTTATGACTGTAGTGGGA
 AACCTTCTTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCATGTATTTTCT
 CTTGGGCAATCTTTCTTCTGACTTTTGTACTCTTCCATCACAGCACCTAGGATGCTGG
 TTGACTTGCTCTCAGGCAACCCTACCATTTCCTTTGGTGGATGCCTGACTCAACTCTTCTTC
 30 TTCCACTTCATTGGAGGCATCAAGATCTTCTGCTGACTGTCATGGCGTATGACCGCTACA
 TTGCCATTTCCCAGCCCCCTGACTACACGCTCATTATGAATCAGACTGTCTGTGCACTCCTT
 ATGGCAGCCTCCTGGGTGGGGGGCTTCATCCACTCCATAGTACAGATTGCATTGACTATCC
 AGCTGCCATTCTGTGGGCCTGACAAGCTGGACAACCTTTTATTGTGATGTGCCTCAGCTGAT
 CAAATTGGCCTGCACAGATACCTTTGTCTTAGAGCTTTTAATGGTGTCTAACAATGGCCTG
 35 GTGACCCTGATGTGTTTTCTGGTGCTTCTGGGATCGTACACAGCACTGCTAGTCATGCTCC
 GAAGCCACTCACGGGAGGGCCGAGCAAGGCCCTGTCTACCTGTGCCTCTCACATTGCTGT
 GGTGACCTTAATCTTTGTGCCTTGCTATACACAATTGTACCCCCATGCTGAATCCTGCCATCTA
 TACCTTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG
 40 ACCCTATTGGTCCCCTGGAGCACAGACCCTTACATTAG (SEQ ID NO: 80)

AOLFR43 sequences:

45 MQKPQLLVPIIATSNGLVHAAVFLLVGIPGLGPTIHFVLAFLPLCFMYALATLGNLTIVLIIRVE
 RRLHEPMYLFLAMLSTIDLVLSSITMPKMASLFLMGIQEIEFNICLAQMFLIHSAVESAVLLA
 MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFPLPFILKWLSYCQHTVTHSFCLHQ
 DIMKLSCTDTRVNVVYGLFIILSVMGVDSLFIGFSYILILWAVLELSSRRAALKAFNTCISHLCAV
 LVFYVPLIGLSVHRLGGPTSLLHVVMANTYLLLPPVNVNPLVYGAKTKEICSRVLCMFSQGGK
 (SEQ ID NO: 81)

50 ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG
 CAGCATACTTCTTTTGGTGGGTATCCCTGGCCTGGGGCCTACCATACACTTTTGGCTGGCT
 TTCCCAGTGTGTTTTATGTATGCCTTGGCCACCCTGGGTAACCTGACCATTGTCTCATCAT
 TCGTGTGGAGAGGCGACTGCATGAGCCCATGTACCTCTTCTGGCCATGCTTTCCACTATT
 GACCTAGTCTCTCTCTATACCATGCCCCAAGATGGCCAGTCTTTTCTGATGGGCATCCA
 55 GGAGATCGAGTTCAACATTTGCCTGGCCCAGATGTTCTTATCCATGCTCTGTGAGCCGTG
 GAGTCAGCTGTCTGCTGGCCATGGCTTTTGACCGCTTTGTGGCCATTTGCCACCCATTGC
 GCCATGCTTCTGTGCTGACAGGGTGTACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG

GGGGTTTGTATTCTTCTTCCCACTGCCCTTCATCCTCAAGTGGTTGTCCTACTGCCAAACAC
ATACTGTACACACTCCTTCTGTCTGCACCAAGATATTATGAAGCTGTCCTGTACTGACAC
CAGGGTCAATGTGGTTTATGGACTCTTCATCATCCTCTCAGTCATGGGTGTGGACTCTCTCT
TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTTGGAGCTGTCCTCTCGGAGGGCA
5 GCACTCAAGGCTTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTTCTATGTACC
CCTCATTGGGCTCTCGGTGGTGCATAGGCTGGGTGGTCCACCTCCCTCCTCCATGTGGTT
ATGGCTAATACCTACTTGTGCTACCACCTGTAGTCAACCCCTTGTCTATGGAGCCAAGA
CCAAAGAGATCTGTTCAAGGGTCTCTGTATGTTCTCACAAAGGTGGCAAGTGA (SEQ ID
NO: 82)

10

AOLFR44 sequences:

MSSCNFTHATFVLIGIPGLEKAHFWVGFPLLSMYVVMFNGNCIVVFIVRTERSLHAPMYLFLC
MLAAIDLALSTSTMPKILALFWFDSREISFEACLQMFHIALSAIESTILLAMAFDRYVAICHPL
RHA AVLNNVT AQIGIVAVVRGSLFFFLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYADTLP
15 NVVYGLTAILVMGVDMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAFYVPLIGLS
VVHRFGNSLHPIVRVVMGDIYLLPPVINPIIYGAKTKQIRTRVLAMFKISCDKDLQAVGGK
(SEQ ID NO: 83)

20

ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA
AAGCCCATTTCTGGGTGGCTTCCCCCTCCTTTCCATGTATGTAGTGGCAATGTTTGGAAAC
TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTTC
TCTGCATGCTTGACGCAATTGACCTGGCCTTATCCACATCCACCATGCCTAAGATCCTTGCC
CTTTTCTGGTTTGATTCCCGAGAGATTAGCTTTGAGGCCTGTCTTACCCAGATGTTCTTTAT
TCATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCCATGGCCTTTGACCGTTATGTGG
25 CCATCTGCCACCCACTGCGCCATGCTGCAGTGCTCAACAATACAGTAACAGCCCAGATTGG
CATCGTGGCTGTGGTCCGCGGATCCCTCTTTTTTTTCCCACTGCCTCTGCTGATCAAGCGGC
TGGCCTTCTGCCACTCCAATGTCCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAA
GTTGGCCTATGCAGACACTTTGCCCAATGTGGTATATGGTCTTACTGCCATTCTGCTGGTC
ATGGGCGTGGACGTAATGTTTCATCTCCTTGTCTATTTTCTGATAATACGAACGGTTCTGC
30 AACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGTGTACACATTGGTGT
GGTACTCGCCTTCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCGCTTTGGAACAGC
CTTCATCCCATTTGTGCGTGTGTGTCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCACTAA
TCCCATCATCTATGGTGGCAAAACCAAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG
ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

35

AOLFR45 sequences:

MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIQADAALHEPMYFLA
MLATIDLVLSSSTLPKMLAIFWFRDQEINFACLVQMFFLHFSIMESAVLLAMAFDRYVAICKP
LHYTTVLTGSLITKIGMAAVARAVTLMTPLPFLRRPHYCRGPVIAHCYCEHMAVVRACGDT
40 SFNNIYGIAVAMFSVLDLLFVILSYVFLQAVLQLASQEARYKAFGTCVSHIGAILSTYTPVVIS
SVMHRVARHAAPRVHILLAIFYLLFPPMVNPIIYGVKTKQIREYVLSLFQRKNM (SEQ ID NO:
85)

45

TGGAAACAAGAGGTAATCTTTGCAGGTGGGATAGCACAGGTTGAACTCTAATCATATATA
CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTCCA
GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTGTGGTAGGAAT
TCCTGGTTTGGAAACACCTGCATGCCTGGATCTCCATCCCTTCTGCTTTGCTTATACTCTGG
CCCTGCTAGGCAACTGTACCCTTCTCTTATTATCCAGGCTGATGCAGCCCTCCATGAACCC
ATGTACCTCTTTCTGGCCATGTTGGCAACCATTGACTTGTTCTTTCTTCTACAACGCTGCC
50 CAAAATGCTTGCCATATTCTGGTTTCAGGGATCAGGAGATCAACTTCTTTGCCTGTCTGGTC
CAGATGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTT
TGACCGCTATGTGGCCATCTGCAAGCCATTGCACTACACGACGGTCCTGACTGGGTCCCTC
ATCACCAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCT
TCCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCCATGCTACTGTGAACA
55 CATGGCTGTGGTAAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATTGCT
GTGGCCATGTTTAGTGTGGTGTGGACCTGCTCTTTGTTATCCTGTCTTATGTCTTCATCCT

TCAGGCAGTTCTCCAGCTTGCCCTCTCAGGAGGCCCGCTACAAAGCATTTGGGACATGTGTG
TCTCACATAGGTGCCATCCTGTCCACCTACACTCCAGTAGTCATCTCTTCAGTCATGCACCG
TGTAGCCCCGCCATGCTGCCCCCTCGTGTCCACATACTCCTTGCTATTTTCTATCTCCTTTTCC
5 CACCCATGGTCAATCCTATCATATATGGAGTCAAGACCAAGCAGATTTCGTGAGTATGTGCT
CAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTTTTTATCCCACTTGCCA
AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAATTGCAGAGT
ATCTTTGACAATTCTCTAGTATGATAAGGAAAATGAGGTTTCATTCCTCACAGATCTACGA
GTCAGGTCAAACCAGGAGTGCACCTATAGTCTGGTCTGATAGTAGAGGTTTGACCTTCCCA
10 TTGTCATAGACTCATCACATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAATCTG
GGTGAAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCCAAACAGCTGAGTC (SEQ ID
NO: 86)

AOLFR46 sequences:

15 MNIKHCGWHMIHTWLNIREDDDSDFKNFIGQIQLSGNPHSTTSRMYFLCFCTSLLGFKVHVW
SRLIXKLYMASPNDSTAPVSEFLICFPNFQSWQHWLSLPLSLLFLLAMGANTLLITIQLEAS
LHQPLYLLSLLSLLDIVLCLTVIPKVLAIWFDFLRSISFPACFLQMFIMNSFLTMESECFMVA
YDRYVAICHPLRYPSTIDQFVARAVVFVIARNAFVSLPVPMLSARLRYCAGNIKNKICSNLSVS
KLSCDDITFNQLYQFVAGWTLGSDLLIVISYFILKVVLRKAEGAVAKALSTCGSHFILILFFS
20 TVLLVLVITNLARKRIPDPVILLNHLHLPALNPVYGVRTKEIKQGIQNLKRL (SEQ ID NO:
87)

ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT
GATGACAGTGATTTTAAAACTTTATTGGACAGATACAGGGCCTCAGTGGAACCCACACT
25 CTACTACGTCTAGAATGTACTTTTTATGTTTCTGTACTTCTCTACTAGGTTTTAAGGTACAC
TGGGTCTCCAGATTGATCANGAACTTTACATGGCATCTCCCAACAATGACTCCACTGCCC
CAGTCTCTGAATTCCTCCTCATCTGCTTCCCCAACTTCCAGAGCTGGCAGCACTGGTTGTCT
CTGCCCCCTCAGCCTTCTCTTCTCCTGGCCATGGGAGCTAACACCACCTCCTGATCACCAT
CCAGCTGGAGGCCTCTCTGCACCAGCCCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGG
30 ACATCGTGCTCTGCCTACCGTCATCCCCAAGGTCCTGGCCATCTTCTGGTTTGACCTCAGG
TCGATCAGCTTCCCAGCCTGCTTCTCCAGATGTTTCATCATGAACAGTTTTTTGACCATGGA
GTCCTGCACGTTTCATGGTCATGGCCTATGACCGTTATGTGGCCATCTGCCATCCATTGAGA
TACCCGTCTATCATCACTGACCAGTTTGTGGCTAGGGCCGTTGGTCTTTGTTATAGCCCGGA
ATGCCTTTGTTTCTCTTCTGTTCCCATGCTTCTGCCAGGCTCAGATACTGTGCAGGAAAC
35 ATAACAAGAAGTGCATGTCAGTAACCTGCTGTGTGCCAAACTCTTGTGATGACATCA
CTTTCAATCAGCTCTACCAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTTATCCTT
ATTGTTATCTCCTATTCTTTTATATTGAAAGTTGTGCTTAGGATCAAGGCCGAGGGTGCTGT
GGCCAAGGCCTTGAGCACGTGTGGTTCCCACTTCATCCTCATCCTCTTCTTCAGCACAGTCC
TGCTGGTTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCCTCCAGATGTCCCCATCCT
40 GCTCAACATCCTGCACCACCTCATTCCCCCAGCTCTGAACCCCATTTGTTATGGTGTGAGA
ACCAAGGAGATCAAGCAGGAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

AOLFR47 sequences:

MSASNITLTHPTAFLLVGIPGLEHLHIWISIPFCLAYTLALLGNCTLLLIQADAALHEPMYLFLA
45 MLAAIDLVLSSSALPKMLAIFWFRDREINFFACLAQMFFLHSFSIMESAVLLAMAFDRYVAICK
PLHYTKVLTGSLITKIGMAAVARAVTLMTPPLPFLRLCFHYCRGPVIAHCYCEHMAVVRLACGD
TSFNNIYGIAMFIVLDLLLVLISYIFILQAVLLLASQEARYKAFGTCVSHIGAILAFYTTVIS
SVMHRVARHAAPHVHILLANFYLLFPPMVNPIHYGVKTKQIRESILGVFPRKDM (SEQ ID NO:
89)

50 ATGTCAGCCTCCAATATCACCTTAACACATCCAACCTGCCTTCTTGTGGTGGGGATTCCAG
GCCTGGAACACCTGCACATCTGGATCTCCATCCCTTTCTGCTTAGCATATACACTGGCCCTG
CTTGGAACCTGCACTCTCCTTCTCATCATCCAGGCTGATGCAGCCCTCCATGAACCCATGT
ACCTCTTTCTGGCCATGTTGGCAGCCATCGACCTGGTCCTTTCCTCCTCAGCACTGCCAAA
ATGCTTGCCATATTCTGGTTTCAGGGATCGGGAGATAAACTTCTTTGCCTGTCTGGCCCAGA
55 TGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTTTGAC
CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGTCCTGACTGGGTCCCTCATCA

CCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCTTCCT
GCTGAGATGTTTCCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGAACACATG
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTGG
CCATGTTTATTGTGGTGTGGACCTGCTCCTTGTATCCTGTCTTATATCTTTATTCTTCAG
5 GCAGTTCTACTGCTTGCCTCTCAGGAGGCCCGCTACAAGGCATTGTTGGGACATGTGTCTCTC
ATATAGGTGCCATCTTAGCCTTCTACACAACCTGTGGTCATCTCTTCAGTCATGCACCGTGTA
GCCCCCATGCTGCCCCCTCATGTCCACATCCTCCTTGCCAATTTCTATCTGCTCTTCCCACC
CATGGTCAATCCCATAATCTATGGTGTCAAGACCAAGCAAATCCGTGAGAGCATCTTGGGA
GTATTCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

10

AOLFR48 sequences:

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL
CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFHLSLGMESTVLLAMAFDRYVAICH
PLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDI
15 RVNVVYGLIVISAIGLDSLLISFSYLLIKTVLGLTREAAQAKAFGTCVSHVCAVFIFYVPFGLSM
VHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVATHASEP (SEQ ID NO:
91)

ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC
20 CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACCTTATTGCT
GTGCTAGGTAACCTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCA
TGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCCC
AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGCTACA
GATGTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCTTTT
25 GACCGCTATGTGGCCATCTGTACCCACTGCGCCATGCCACAGTACTTACGTTGCCTCGTG
TCACCAAAATTGGTGTGGCTGCTGTGGTGCAGGGGGCTGCACTGATGGCACCCTTCCTGT
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCCTACACC
AAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCCTTATCGT
CATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGCTTATTCTTA
30 AGACTGTGTTGGGCTTGACACGTGAAGCCCAGGCCAAGGCATTTGGCACTTGCGTCTCTCA
TGTGTGTGCTGTGTTTATATTCTATGTACCTTTCATTGGATTGTCCATGGTGCATCGCTTGA
GCAAGCGGCGTGACTCTCCGCTGCCCCGTCATCTTGCCCAATATCTATCTGCTGGTTCCTCCT
GTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAGGAGATTGACAGCGCATCCTTCGA
CTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

35

AOLFR49 sequences:

MLTFHNVCSPSSFWLTGIPGLESLSHVWLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF
LCMLAAIDLVLSTSTIPKLLGIFWFGACDIGLDAQLGQMFLIHCFAVESGIFLAMAFDRYVAIC
NPLRHSMLVLTYYTVVGRGLVLSLLRGVLVYIGPLPLMIRLRLPLYKTHVISHSYCEHMAVVALT
40 GDSRVNNVYGLSIGFLVLILDSVAIAASYVMIFRAVMGLATPEARLKTGTCASHLCAILIFYVP
IAVSSLIHRFGQCVPPPVTLLANFYLLIPPILNPVYAVRTKQIRESLLQIPRIEMKIR (SEQ ID
NO: 93)

ATGCTCACTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG
45 GCTGGAGTCCCTACACGTCTGGCTCTCCATCCCCTTTGGCTCCATGTACCTGGTGGCTGTG
GTGGGGAATGTGACCATCCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACCAGCCCATG
TACTTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTTCTGTCTACTTCCACTATACCCAA
ACTTCTGGGAATCTTCTGGTTCGGTGTGTTGACATTGGCCTGGACGCTTGGGCCAA
ATGTTCTTATCCACTGCTTTGCCACTGTTGAGTCAGGCATCTTCCTTGCCATGGCTTTTGA
50 TCGCTACGTGGCCATCTGCAACCCACTACGTCATAGCATGGTGCTCACTTATACAGTGGTG
GGTCTGTTTGGGGCTTGTCTCTCCTCCGGGTGTTCTCTACATTGGACCTCTGCCTCTGAT
GATCCGCTGCGGCTGCCCTTTATAAAACCCATGTTATCTCCCACTCCTACTGTGAGCAC
ATGGCTGTAGTTGCCTTGACATGTGGCGACAGCAGGGTCAATAATGTCTATGGGCTGAGC
ATCGGCTTCTGGTGTGATCCTGGACTCAGTGGCTATTGCTGCATCCTATGTGATGATTTT
55 CAGGGCCGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAACCCCTGGGGACATGCGC
TTCTCACTCTGTGCCATCCTGATCTTTTATGTTCCCATGCTGTTTCTTCCCTGATTACCG

ATTTGGTCAGTGTGTGCCTCCTCCAGTCCACACTCTGCTGGCCAACTTCTATCTCCTCATTC
CTCCAATCCTCAATCCCATTGTCTATGCTGTTTCGCACCAAGCAGATCCGAGAGAGCCTTCT
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

5 **AOLFR50 sequences:**

MNLDSSFFSFLKSLIMALSNSSWRLPQPSFFLVGIPGLEESQHWIALPLGILYLLALVGNVTILFII
WMDPSLHQSMYLFLSMLAAIDLVAASSTAPKALAVLLVRAQEIGYTVCLIQMFTHAFSSMES
GVLVAMALDRYVAICHPLHHSTILHPGVIGHIGMVVLVRGLLLIPFLILLRKLIFCQATIIGHAY
CEHMAVVKLACSETTVNRAYGLTVALLVVGDLVLAIGVSYAHILQAVLKVPNEARLKAFST
10 CGSHVCVILVFYIPGMFSFLTHRFGHVPHHVHLLAILYRLVPPALNPLVYRVKTQKIHQ
(SEQ ID NO: 95)

ATGAATTTGGATTCTTTTTTCTCTTTCCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC
CAGCTGGAGGCTACCCCAGCCTTCTTTTTCTCTGGTAGGAATCCGGGTTTAGAGGAAAGC
15 CAGCACTGGATCGCACTGCCCCGCGCATCCTTTACCTCCTTGCTCTAGTGGGCAATGTTA
CCATTCTCTTCATCATCTGGATGGACCCATCCTTGACCAATCTATGTACCTCTTCTGTCC
ATGCTAGCTGCCATCGACCTGGTTGTGGCCTCCTCCACTGCACCCAAAGCCCTTGCACTGC
TCCTGGTTCGTGCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTTACCCAT
GCATTCTCCTCCATGGAGTCAGGGGTACTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA
20 TTTGTCACCCCTTGACCATTCACAATCCTGCATCCAGGGGTCATAGGGGCACATCGGAAT
GGTGGTGTGGTGCGGGGATTACTACTCCTCATCCCCTTCTCATTCTGTTGCGAAAACCTT
ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAAC
TTGCTGCTCAGAAACCACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGCTTGTGGT
TGGGCTGGATGTCTGGCCATTGGTGTTCCTATGCCACATTCTCCAGGCAGTGTGAAG
25 GTACCAGGAAATGAGGCCCCGAACTTAAGGCCTTTAGCACATGTGGCTCTCATGTTGTGTCA
TCCTGGTCTTCTATATCCCAGGAATGTCTCCTTCTCCTCACTACCGCTTGGTCATCATGTA
CCCCATCACGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGTGCCACCTGCACTCAATCC
TCTTGTCTATAGGGTGAAGACCCAGAAGATCCACCAGTGA (SEQ ID NO: 96)

30 **AOLFR51 sequences:**

MCQQILRDCILLIHLHCINRKKVSLVMLGPAYNHTMETPASFLLVGIPGLQSSHLWLAIISLAM
YIIALLGNTIIVTAIWMDSRHEPMYCFLCVLAADVIMASSVVPKMVSIFCSGDSSISFSACFTQ
MFFVHLATAVETGLLLTMAFDRYVAICKPLHYKRILTPQVMLGMSMAITIRAIITPLSWMVS
HLPFCGSNVVVHSYCEHIALARLACADPVPSSLYSLIGSSLMVGSVDVAFIAASYILILKAVFGLSS
35 KTAQLKALSTCGSHVGMALYYLPGMASIYAAWLGDVVPPLHTQVLLADLYVIIPATLNPIIY
GMRTKQLRERIWSYLMHVLFHDHNSLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
40 CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTACATCTTTGGCTGGCTATCTCACTGA
GTGCCATGTACATCATAGCCCTGTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
45 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
GCAGTCTCTACAGCTGATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
50 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
AGCATTAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACCCCAAGTCCTGC
TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
CAAACAACCTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
55 CTGGGTTTCATGA (SEQ ID NO: 98)

AOLFR52 sequences:

MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAMYITALLGNTLIVTAIWMDSTRHEPMY
CFLCVLAAVDIVMASSVVPKMVSIFCSGSSISFSACFTQMFFVHLATAVETGLLLTMAFDYRV
AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMTPLSWMMNHLPCGSNVVVHSYCKHIALAR
5 LACADPVPSLSYSLIGSSLMVGSVDVAFIAASYILILRAVFDLSSKTAQLKALSTCGSHVGVMA
YLPGMASIYAAWLGQDIVPLHTQVLLADLYVIIPATLNPIHYGMRTKQLLEGIWSYLMHFLFDH
SNLGS (SEQ ID NO: 99)

ATGCTGGGTCCAGCTTACAACCACACAATGGAAACCCCTGCCTCCTTCCTCCTTGTGGGTA
10 TCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC
AGCCCTGTTAGGAAACACCCTCATCGTGACTGCAATCTGGATGGATTCCACTCGGCATGAG
CCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTATGGCCTCCTCCGTGGT
ACCCAAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTGTTC
ACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATGG
15 CTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCACGCCTCA
AGTGATGCTGGGAATGAGTATGGCCGTCACCATCAGAGCTGTCACATTCATGACTCCACTG
AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTTGTCCACTCCTACTGTAA
GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCAGCAGTCTCTACAGTCTG
ATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCTGCCTCCTATATCTTAAT
20 TCTCAGGGCAGTATTTGATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAAGCACATGT
GGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATGGCATCCATCTATGCGG
CCTGGTTGGGGCAGGATATAGTGCCCTTGACACACCCAAGTGCTGCTAGCTGACCTGTACGT
GATCATCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAACAATTGCTGGAG
GGAATATGGAGTTATCTGATGCACTTCCTCTTTGACCACTCCAACCTGGGTTCATGA (SEQ
25 ID NO: 100)

AOLFR54 sequences:

MSDSNLSDNHLPDFTFFLTGIPGLEAAHFWIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY
LFLCLLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMAFDRYVA
30 ICNPLRYTTILNHAVIGRIGFVGLFRSVAIVSPFIILLRRLPYCGHRVMTHTYCEHMGARLACA
NITVNIVYGLTVALLAMGLDSILIAISYGFIHAVFHLPSHDAQHKALSTCGSHIGILVFYIPAFF
SFLTHRFGHHEVPKHVHIFLANLYVLVPPVLNPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID
NO: 101)

ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC
35 CAGGGCTGGAGGCTGCCCACTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTTGTAGC
ACTGGTTGGAAATGCTGCCCTCATCCTGGTCATTGCCATGGACAATGCTCTTCATGCACCT
ATGTACCTCTTCTCTGCTTCTCTCACTCACAGACCTGGCTCTCAGTTCTACCACTGTGCC
CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCTTTTGGTGGATGCCTGGCC
40 CAGATGTTTTGTGTCCATTCTATCTATGCTCTGGAGTCCTCGATTCTACTTGCCATGGCCTT
TGATAGGTATGTGGCTATCTGTAACCCATTAAAGGTATACAACCATTTCAACCATGCTGTC
ATAGGCAGAATTGGCTTTGTGGGCTATTCCGTAAGTGTGGCTATTGTCTCCCCCTTCATCTT
CTTGCTGAGGCGACTCCCTACTGTGGTCACCGTGTGTCATGACACACACATACTGTGAGCAT
ATGGGCATCGCCCGACTGGCCTGTGCCAACATCACTGTCAATATTGTCTATGGGCTAACTG
45 TGGCTCTGCTGGCCATGGGACTGGATTCCATTCTCATTGCCATTTCTATGGCTTTATCCTC
CATGCAGTCTTTACCTTCCATCTCATGATGCCAGCACAAAGCTCTGAGTACCTGTGGCT
CCCACATTGGCATCATCCTGGTTTTCTACATCCCTGCCTTCTTCTCCTTCCTCACCACCGC
TTTGGTCAACCACGAAGTCCCCAAGCATGTGCACATCTTTCTGGCTAATCTCTATGTGCTGG
TGCCTCCTGTACTCAATCCTATTCTCTATGGAGCTAGAACCAAGGAGATTCGGAGTCGACT
50 TCTAAACTGCTTCACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

AOLFR57 sequences:

MSFQVTYMFYLHWTMEKSNNSTLFILLGFSQKNIEVLCFVLFVFCYIAIWMGNLLIMISITCTQ
LIHQPMYFFLNLYLSLDLCYTSTVTPKLMVDLLAERKTISYNNCMIQLFTTHFFGGIEIFILTM
55 AYDRYVAICKPLHYTHMSRQKCNTHIVCCTGGFIHSASQFLLTIFVPFCGPNEIDHYFCDVYPLL
KLACSNHIMIGLLVIANSGLIALVTFVVLVLSYVFILYTIRAYSAERRSKALATCSSHVIVVVLFF

APALFIYIRPVTTFSSEKVFALFYTHIAPMFNPLIYTLRNTEMKNAMRKVWCCQILLKRNQLF
(SEQ ID NO: 103)

5 ATGTCATTTTCAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAAGCAATAATA
GCACTTTGTTTATTCTCTTGGGGTTTTCCCAAATAAGAACATTGAAGTCCTCTGCTTTGTA
TTATTTTGTGTTTGCTACATTGCTATTTGGATGGGAAACTTACTCATAATGATTTCTATCAC
GTGCACCCAGCTCATTACCAACCCATGTATTTCTTCTCAATTACCTCTCACTCTCCGACC
TTTGCTACACATCCACAGTGACCCCCAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC
CATTTCCTATAATAACTGTATGATACAACCTCTTACCACCCATTTTTTTGGAGGCATAGAGA
10 TCTTCATTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTTGCAAGCCCCTGCACTA
CACCATTATTATGAGCAGGCAAAAGTGTAACACAATCATCATAGTTTGTGTACTGGGGGA
TTATACATTCTGCCAGTCAGTTTCTTCTCACCATCTTTGTACCATTTGTGGCCCAATGA
GATAGATCACTACTTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA
TGATAGGTCTCTTAGTCATTGCTAATTCAGGCTTAATTGCTTTGGTGACATTTGTTGTCTTG
15 TTGTTGTCTTATGTTTTATATTGTATACCATCAGAGCATACTCTGCAGAGAGACGCAGCA
AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCCTGTTTTTGTCTCTGCATTG
TTCATTTACATTAGACCGGTCACAACATTCTCAGAAGATAAAGTGTTGCCCTTTTTTATAC
CATCATTGCTCCCATGTTCAACCCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC
GCCATGAGGAAAGTGTTGGTGTGTCAAATACTCCTGAAAAGAAATCAACTTTTCTGA (SEQ
20 ID NO: 104)

AOLFR58 sequences:

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQNPVQEIIVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGLSFLDACFSSVI
25 TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCPLYLLELACTDTHIFGLMVVINS
FICIINFSLLLVSAYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 105)

30 ATGTTCTCAATGACAACAGAAGCACTCAATAATTTGCACTTGGATGTACCAACTTGTTAA
TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCCTTTGTCCTAATTGCAGACTATA
CATGATCCCTGTTGGAGCTTTTCATCTTTTCCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCCTGGGACTTTACAGAATCCAAATGTTTCAGGAAATAGTATTTGTTG
TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATCTC
35 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCCTGTCCTTCTGGA
TGCGTGCTTCTCATCTGTCATACCCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
40 GGCCTCTTGCAATCCATGATACAAATCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTCTCTTGTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA
45 TATTTGTATATACACGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTACACTTTCAGGAATAAGGAAGTAAAC
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 106)

AOLFR59 sequences:

MGDWNNSDAVEPIFILRGFPGLLEYVHWSLSILFCLAYLVAFMGNVTILSVIWISSLHQPMYYFI
SILAVNDLGMSTLPTMLAVLWDAPEIQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH
PLHYPTILTNSVIGKIGLACLLRSLGVVLPPTLLLRHYHYCHGNALSHAFCLHQDVLRLSCTDA
RTNSIYGLCVVIATLGVDISYVLLINTVLDIASREEQLKALNTCVSHICVVLFFVPVIGVS
55 MVHRFGKHLSPIVHILMADIYLLPPVLNPIVYSVRTKQIRLGILHKFVLRRLF (SEQ ID NO:
107)

ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTTCTG
 GACTGGAGTATGTTCACTTCTGGCTCTCCATCCTCTTCTGTCTTGCATATTTGGTAGCATTT
 ATGGGTAATGTTACCATCCTGTCTGTCAATTTGGATAGAATCCTCTCTCCATCAGCCCATGTA
 5 TTACTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTTCCCACCA
 TGCTTGCTGTGTTATGGTTGGATGCTCCAGAGATCCAGGCAAGTGCTTGCTATGCTCAGCT
 GTTCTTCATCCACACATTACATTCCTGGAGTCCTCAGTGTTGCTGGCCATGGCCTTTGACC
 GTTTTGTTGCTATCTGCCATCCACTGCACTACCCACCATCCTCACCAACAGTGTAATTGGC
 AAAATTGGTTTGGCCTGTTTGCTACGAAGCTTGGGAGTTGTACTTCCCACACCTTTGCTACT
 10 GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTCACGCCTTCTGTTTGCACCAGGAT
 GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA
 TTGCCACACTAGGTGTGGATTCAATCTTCATACTTCTTTCTTATGTTCTGATTCTTAATACT
 GTGCTGGATATTGCATCTCGTGAAGAGCAGCTAAAGGCACTCAACACATGTGTATCCCATA
 TCTGTGTGGTGTCTTCTTTGTGCCAGTTATTGGGGTGTCAATGGTCCATCGCTTTGGG
 15 AAGCATCTGTCTCCCATAGTCCACATCCTCATGGCAGACATCTACCTTCTTCTCCCCCAGT
 CCTTAACCCTATTGTCTATAGTGTGAGAACAAGCAGATTTCGTCTAGGAATTCTCCACAAG
 TTTGTCCTAAGGAGGAGGTTTAA (SEQ ID NO: 108)

AOLFR60 sequences:

20 MFLPNDTQFHPSSFLLLGIPGLETLHIWIGFPFCVYMIALIGNFTILLVIKTDSSLHQPMFYFLA
 MLATTDVGLSTATIPKMLGIFWINLRGIIEACLQMFHNFNFTLMESAFLVAMAYDSYVAICN
 PLQYSAILTNKVSVIGLVFVRALIFVIPSILLRLPFCGNHVIPHTYCEHMGHLHLSCASIKINI
 IYGLCAICNLVFDITVIALSYVHILCAVFRLPHTHEPRLKSLSTCGSHVCVILAFYTPALFSFMTHC
 FGRNVPRYIHILLANLYVVVPPMLNPVIYGVRTKQIYKCVKKILLQEQGMEKEEYLIHTRF
 25 (SEQ ID NO: 109)

ATGTTCTTCCCAATGACACCCAGTTTACCCCTCCTCCTTCTGTTGCTGGGGATCCCAGG
 ACTAGAAACACTTCACATCTGGATCGGCTTTCCCTTCTGTGCTGTGTACATGATCGCACTC
 ATAGGGAACCTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCCTACACCAGCCCATGT
 30 TCTACTTCTGGCCATGTTGGCCACCACTGATGTGGGTCTCTCAACAGCTACCATCCCTAA
 GATGCTTGGAATCTTCTGGATCAACCTCAGAGGGATCATCTTTGAAGCCTGCCTCACCCAG
 ATGTTTTTTATCCACAACCTTCACTTATGGAGTCAGCAGTCCTTGTGGCAATGGCTTATG
 ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCCTCACCAACAAGGTTGT
 TTCTGTGATTGGTCTTGGTGTGTTTGTGAGGGCTTTAATTTTCGTCACTCCCTCTATACTTC
 35 TTATATTGCGGTTGCCCTTCTGTGGGAATCATGTAATTCCCCACACCTACTGTGAGCAT
 GGGCTTGCTCATCTATCTTGTGCCAGCATCAAAATCAATATTATTTATGGTTTATGTGCCA
 TTTGTAACTGGTGTGTTGACATCACAGTCATTGCCCTCTCTTATGTGCATATTCTTTGTGCT
 GTTTTCCGTCTTCTACTCATGAGCCCCGACTCAAGTCCCTCAGCACATGTGGTTCACATGT
 GTGTGTAATCCTTGCCCTTCTATACACCAGCCCTCTTTTCCCTTTATGACTCATTGCTTTGGCC
 40 GAAATGTGCCCCGCTATATCCATATACTCCTAGCCAATCTCTATGTTGTGGTGCCACCAAT
 GCTCAATCCTGTCATATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAT
 ATTATTGCAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA
 (SEQ ID NO: 110)

AOLFR61 sequences:

45 MSIINTSYVEITTFVLVGMPTGLEAYAHIWISIPICSMYLIAILGNGTILFIKTEPSLHGPMYYFLSML
 AMSDLGLSLSSLPTVLSIFLNAPETSSSACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYT
 SILTTVRVAQIGIVFSFKSMLLVLPFPFTLRSLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
 GFFGALCLMVDFILIAVSYTLILKTVPPIASKKEELKALNTCVSHICAVIIFLPIINLAVVHRFAG
 50 HVSPLINVLMANVLLLVPPLMKPIVYCVKTKQIRVRVVAKLCQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACACCTTCTTCTTGGTTGGGATGCCAG
 GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
 CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCATGT
 55 ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTATCATCTCTGCCCACT
 GTGTTAAGCATCTTCTGTTCAATGCCCTGAAACTTCTTCTAGTGCCTGCTTTGCCCAGGA

ATTCTTCATTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCATTTGATA
 GATTCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
 5 TAAGAAGCTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCCTACTGTCTCCACCAGGA
 TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
 CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
 ACCGGGAATTGCATCCAAAAAGGAGGAGCTTAAGGCTCTCAATACTTGTGTTTCACACATC
 TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCGG
 10 GCATGTCTCTCCCTCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCGCTGA
 TGAAACCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
 GTGTCAATGGAAGATTTAA (SEQ ID NO: 112)

AOLFR62 sequences:

MFYHNKSFHPVTFFLIGIPGLEDFHWMISGPFCSVYLVALLG NATILLVIKVEQTLREPMFYFL
 15 AILSTIDLALSATSVPRMLGIFWFDAHEINYGACVAQMFLIHAFTGMEAEVLLAMAFDRYVAIC
 APLHYATILTSVLVGISMCIVIRPVLLTLP MVYLIYRPLFCQAHIIAHSYCEHMGIAKLSCGNIRI
 NGIYGLFVVVSFFVLNLVLIGISYVYILRAVFRLP SHDAQLKALSTCGAHVGVICVFYIPSVFSFLT
 HRFQHQIPGYIHILVANLYLIIPPSLNP IYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

20 ATGTTTTATCACAACAAGAGCATATTTACCCAGTCACATTTTTCTCATTGGAATCCCAGG
 TCTGGAAGACTTCCACATGTGGATCTCCGGGCCTTTCTGCTCTGTTTACCTTGTGGCTTTGC
 TGGGCAATGCCACCATCTGCTAGTCATCAAGGTAGAACAGACTCTCCGGGAGCCCATGTT
 CTACTTCTCGCCATTCTTTCCACTATTGATTGGCCCTTTCTGCAACCTCTGTGCCTCGCA
 25 TGCTGGGTATCTTCTGGTTTGTATGCTCAGGAGATTAACTATGGAGCTTGTGTGGCCAGAT
 GTTCTGATCCATGCCTTCACTGGCATGGAGGCTGAGGTCTTACTGGCTATGGCTTTTGAC
 CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATCTTGACATCCCTAGTGTTGGT
 GGGCATTAGCATGTGCATTGTAATTCGTCCCGTTTTACTTACACTTCCCATGGTCTATCTTA
 TCTACCGCCTACCCTTTTGTGAGGCTCACATAATAGCCCATTCCTACTGTGAGCACATGGG
 30 CATTGCAAAAATTGTCCTGTGGAAACATTCGTATCAATGGTATCTATGGGCTTTTTGTAGTTT
 CTTTCTTTGTTCTGAACCTGGTGCTCATTGGCATCTCGTATGTTTACATTCTCCGTGCTGTC
 TTCCGCCTCCCATCACATGATGCTCAGCTAAAAGCCCTAAGCACGTGTGGCGCTCATGTTG
 GAGTCATCTGTGTTTTCTATATCCCTTCAGTCTTCTCTTTCCTTACTCATCGATTTGGACAC
 CAAATACCAGGTTACATTACATTCTTGTGGCAATCTCTATTTGATTATCCCACCTCTCT
 35 CAACCCCATCATTTATGGGGTGAGGACCAAACAGATTCGAGAGCGAGTGCTCTATGTTTTT
 ACTAAAAAATAA (SEQ ID NO: 114)

AOLFR63 sequences:

MSIINTSYVEITTFVLVGMPLGEYAHIWISIPICSMYLIAILGNGTILFIKTEPSLHEPMYYFLSML
 40 AMSDLGLSLSSLPTVLSIFLNFNAPEISSNACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYTS
 ILTTVRVAQIGIVFSFKSMLLVLPFPFTLRNLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
 GFFGALCLMVDFILIAVSYTLILKTVLGIASKKEQLKALNTCVSHICAVIIFYLPIINLAVVHRFAR
 HVSPLINVLMANVLLLVPPLTNPIVYCVKTKQIRVRVVAKLCQRKI (SEQ ID NO: 115)

45 ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
 GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
 CTAGGAAATGGCACCATTCTTTTTATCATCAAGACAGAGCCCTCCTTGCATGAGCCCATGT
 ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT
 GTGTTAAGCATCTTCTGTTCAATGCTCCTGAAATTTATCCAATGCCTGCTTTGCCAGGA
 50 ATTCTTCATTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCATTTGATA
 GATTCTAGCCATCCACAACCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
 TAAGAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCCTACTGTCTCCACCAGGA
 TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
 CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
 55 ACTGGGAATTGCATCCAAAAAGGAGCAGCTTAAGGCTCTCAATACTTGTGTTTCACACATC
 TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG

GCATGTCTCTCCCCCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGA
CGAACCCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAATT
GTGTCAACGGAAGATTTAA (SEQ ID NO: 116)

5 **AOLFR64 sequences:**

MTILLNSSLQRATFFLTGFQGLEGLHGWISIPFCFIYLTVILGNLTILHVICTDATLHGPMYYFLG
MLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPL
HDSTVLTPACIVKMGLSSVLRALLILPLPFLLRQYCHSHVLAHAYCLHLEIMKLACSSIIVN
HIYGLFVVACTVGVDLLIFLSYALILRTVLSIASHQERLRALNTCVSHICAVLLFYIPMIGLSLV
10 HRFGEHLPRVVHLFMSYVYLLVPPLMNPIIYSIKTKQIRQRIKKFQFIKSLRCFWKD (SEQ ID
NO: 117)

ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTTCTTCCTGACGGGCTTCCAAG
GTCTAGAAGGCTCCCATGGCTGGATCTCTATTCCCTTCTGCTTCATCTACCTGACAGTTATC
15 TTGGGGAACCTCACCATTCTCCACGTCATTTGTAAGTATGATGCCACTCTCCATGGACCCATGT
ACTATTTCTTGGGCATGCTAGCTGTACAGACTTAGGCCTTTGCCTTTCCACACTGCCCCACT
GTGCTGGGCATTTTCTGGTTTGATACCAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGC
TCTTCTTCATCCACACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGAC
CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCCTGACACCTGCATGTATTG
20 TCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCCTTGCCATTCTC
CTGAAGCGCTTCCAATACTGCCACTCCCATGTGCTGGCTCATGCTTATTGTCTTCACCTGGA
GATCATGAAGCTGGCCTGCTCTAGCATCATTGTCAATCACATCTATGGGCTCTTTGTTGTG
GCCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTCTCTCATACGCCCTCATCTTCGCAC
CGTGCTCAGCATGCTTCCACCAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT
25 ATCTGTGCTGTACTGCTCTTCTACATCCCCATGATTGGCTTGTCTCTTGTGCATCGCTTTGG
TGAACATCTGCCCCGCGTTGTACACCTCTTCATGTCTATGTGTATCTGCTGGTACCACCCC
TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTCGCCAGCGCATCATTAAGAA
GTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGAAGGATTAA (SEQ ID NO: 118)

30 **AOLFR65 sequences:**

MAGRMSTSNHTQFHPSSFLLLGIPGLEDVHIWIGVPPFFVYLVALLGNTALLFVIQTEQSLHEPM
YYFLAMLDSIDLGLSTATIPKMLGIFWFNTKEISFGGCLSHMFFIHFHTAMESIVLVAMAFDRYI
AICKPLRYTMILTSKISLIAGIAVLRSLYMVVPLVFLRLPFCGHRIPHTYCEHMGIARLACAS
IKVNIRFGLGNISLLLDVILILSYVRILYAVFCLPSWEARLKALNTCGSHIGVILAFFTPAFFSFL
35 THRFGHNIPQYIHIILANLYVVVPPALNPVIYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCCATCCTTCTTCATTCTCCTACTGCT
GGGTATCCCAGGGCTAGAAGATGTGCACATTTGGATTGGAGTCCCTTTTTCTTTGTGTAT
CTTGTGTGACTCCTGGGAAACACTGCTCTCTTGTGTTGTGATCCAGACTGAGCAGAGTCTCC
40 ATGAGCCTATGTACTACTTCTGGCCATGTTGGATTCCATTGACCTGGGCTTGTCTACAGC
CACCATCCCCAAAATGTTGGGCATCTTCTGGTTCAATACCAAAGAAATATCTTTTGGAGGC
TGCCTTTCTCACATGTTCTTCATCCATTTCTTCACTGCTATGGAGAGCATTGTGTTGGTGGC
CATGGCCTTTGACCGCTACATTGCCATTTGCAAACCTCTTCGGTACACCATGATCCTCACCA
GCAAATCATCAGCCTCATTGCAGGCATTGCTGTCTGAGGAGCCTGTACATGGTGTGTTCC
45 ACTGGTGTTTCTCCTTCTGAGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTTATT
GTGAGCACATGGGCATTGCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTTTGG
CCTTGGCAACATATCTCTCTTGTACTGGATGTTATCCTTATTATTCTCTCCTATGTGAGGA
TCCTGTATGCTGTCTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGT
GGTTCTCATATTGGTGTATCTTAGCCTTTTACACACCATTTTTCATTCTTGACACA
50 TCGTTTTGGCCATAATATCCCACAGTATATACATATTATATTAGCCAACCTGTATGTGGTTG
TCCCACCAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTTCGAGAGAGAG
TGCTGAGGATTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

AOLFR66 sequences:

55 MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDEALHRPMYVFL
ALLSFTDVLMTSTLPTNLFILWFNLKEIDFKACLAQMFFVHTFTGMESGVLMMLALDHCVAI

CFPLRYATILTNSVIAKAGFLTFLRGVMLVIPSTFLTKRLPYCKGNVIPHTYCDHMSVAKISCGN
VRVNAIYGLIVALLIGGFDILCITISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLTYVPAFF
TFFTHHFGGHTIPLHIHIIMANLYLLMPPTMNPVYGVKTRQVRESVIRFFLKGDNSHNF (SEQ
ID NO: 121)

5
ATGTCATTTCTAAATGGCACCAGCCTAACTCCAGCTTCATTCATCCTAAATGGCATCCCTG
GTTTGAAGATGTGCATTTGTGGATCTCCTTCCCACTGTGTACCATGTACAGCATTGCTATT
ACAGGGAACCTTCGGCCTTATGTACCTCATCTACTGTGATGAGGCCTTACACAGACCTATGT
10 ATGCTCTTCCCTTGCCCTTCTTCCCTTCACAGATGTGCTCATGTGCACCAGCACCTTCCCAAC
ACTCTCTTCATATTGTGGTTTAACTCAAGGAGATTGATTTTAAAGCCTGCCTCGCCCAGAT
GTTCTTTGTGCACACCTTCACAGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGAC
CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCCTCACTAATTCAGTCATTGC
TAAAGCTGGGTTCCCTCACTTTTCTTAGGGGTGTGATGCTTGTATCCCTTCCACTTTCCCTCA
CCAAGCGCCTTCATACTGCAAGGGCAACGTCATACCCACACCTACTGTGACCACATGTC
15 TGTGGCCAAGATATCTTGTGGTAATGTCAGGGTTAACGCCATCTATGGTTTGATAGTTGCC
CTGCTGATTGGGGGCTTTGATATCCTGTGCATTACAATCTCCTACACTATGATTCTTCAAGC
AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCTTCAGCACCTGCATGCCCCAC
TTCTGTGCCATAGTCCTCACCTATGTTCCAGCCTTCTTTACCTTCTTTACACACCATTTTGG
GGGACACACCATTCTCTACACATACATATTATTATGGCTAATCTCTACCTACTAATGCCTC
20 CCACAATGAACCCTATTGTGTATGGGGTGAAAACCAGGCAGGTACGAGAAAGTGTCTTA
GGTTCTTTCTTAAGGGAAAGGACAATTCTCATAACTTTTAA (SEQ ID NO: 122)

AOLFR67 sequences:

MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYIIAVVGNCGLICLISHEEALHRPMMYYFLA
25 LLSFTDVTLCCTTMVPMNLCIFWFNLKEIDFNACLAQMFVHMLTGMEGVLMLMALDRYVAI
CYPLRYATILNPNVIAKAGLATFLRNVMILPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN
FKVNAIYGLMVALLIGVFDICISVSYTMILQAVMSLSSADARHKAFTSTCTSHMCSIVITYVAAF
FTFFTHRFVGHNPNIHIIIVANLYLLLPPTMNPVYGVKTKQIQEGVIKFLLDGKVSFTYDK
(SEQ ID NO: 123)

30
ATGTCTGGGGACAACAGCTCCAGCCTGACCCAGGATTCTTTATCTTGAATGGCGTTCCTG
GGCTGGAAGCCACACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTGCTGTC
GTGGGGAACCTGTGGGCTCATCTGCCTCATCAGCCATGAGGAGGCCCTGCACCGGCCCATGT
ACTACTTCCTGGCCCTGCTCTCCTTCACTGATGTACCTTGTGCACCACCATGGTACCTAAT
35 ATGCTGTGCATATTCTGGTTCAACCTCAAGGAGATTGACTTTAACGCCTGCCTGGCCCAGA
TGTTTTTTGTCCATATGCTGACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGA
CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCCTTACCAACCCTGTCATCG
CCAAGGCTGGTCTTGCCACCTTCTTGAGGAATGTGATGCTCATCATCCCATTCCTCTCCTC
ACCAAGCGCCTGCCCTATTGCCGGGGGAACCTCATCCCCACACCTACTGTGACCATATGT
40 CTGTGGCCAAGGTATCCTGTGGCAATTTCAAGGTCAATGCTATTTATGGTCTGATGGTTGC
TCTCCTGATTGGTGTGTTTGATATCTGCTGTATCTCTGTATCTTACACTATGATTTTGCAGG
CTGTTATGAGCCTGTCATCAGCAGATGCTCGTCACAAAGCCTTCAGCACCTGCACATCTCA
CATGTGTTCCATTGTGATCACCTATGTTGCTGCTTTTTTCACTTTTTTCACTCATCGTTTTGT
AGGACACAATATCCCAAACCACATACATCATCGTGGCCAACCTTTATCTGCTACTGCCT
45 CCTACCATGAACCCAATTGTTTATGGAGTCAAGACCAAGCAGATTGAGGAAGGTGTAATTA
AATTTTTACTTGAGACAAGGTTAGTTTTACCTATGACAAATGA (SEQ ID NO: 124)

AOLFR68 sequences:

MTTHRNDTLSTEASDFLLNCFVRSPSWQHWLSLPLSLLFLLAVGANTTLLMTIWLEASLHQPL
50 YYLLSLLSLLDIVLCLTVIPKVLTFWFDLRPISFPACFLQMYIMNCFAMESCTFMVMAVDYR
VAICHPLRYSIITDHFVVKAAAMFILTRNVMLTLPILSAQLRYCGRNVIENCANMSVSRLSC
DDVTINHLVYQFAGGWTLGSDLILFLSYTFILRAVRLKAEGAVAKALSTCGSHFMLILFFSTIL
LVFVLTHVAKKKVSPDVPVLLNVLHHVIPALNPHYGVRTQEIKQGMQRLLKKGK (SEQ ID
NO: 125)

55

ATGACAACACACCGAAATGACACCCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT
 TTGTCAGATCCCCAGCTGGCAGCACTGGCTGTCCCTGCCCCCTCAGCCTCCTTTTCCTCTTG
 GCCGTAGGGGCCAACACCACCCTCCTGATGACCATCTGGCTGGAGGCCTCTCTGCACCAGC
 CCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGGACATCGTGCTCTGCCTCACTGTCATC
 5 CCAAGGTCTGACCATCTTCTGGTTTGACCTCAGGCCCATCAGCTTCCTGCCTGCTTCCT
 CCAGATGTACATCATGAATTGTTTCCTAGCCATGGAGTCTTGACATTCATGGTCATGGCC
 TATGATCGTTATGTAGCCATCTGCCACCCACTGAGATATCCATCAATCATCACTGATCACTT
 TGTAGTCAAGGCTGCCATGTTTATTTTGACCAGAAATGTGCTTATGACTCTGCCCATCCCC
 ATCCTTTCAGCACAACTCCGTTATTGTGGAAGAAATGTCATTGAGAACTGCATCTGTGCCA
 10 ATATGCTCTGTTTCCAGACTCTCCTGCGATGATGTCACCATCAATCACCTTTACCAATTTGCT
 GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTTCTCTCTACACCTTCATTCT
 GCGAGCTGTGCTGAGACTCAAGGCAGAGGGTGCCGTGGCAAAGGCCCTAAGCACATGTGG
 CTCCCACTTCATGCTCATCCTCTTCTTCAGCACCATCCTTCTGGTTTTTGTCTCACACATGT
 GGCTAAGAAGAAAGTCTCCCCTGATGTGCCAGTCTTGCTCAATGTTCTCCACCATGTCATT
 15 CCTGCAGCCCTTAACCCCATCATTTACGGGGTGAGAACCCAAGAAATTAAGCAGGGAATG
 CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

AOLFR69 sequences:

MSYSIYKSTVNIPLSHGVVHSFCHNMNCNFMHIFKFLVDFNMKNVTEVTLFVLKGFTDNLELQ
 20 TIFFFLFLAIYLFITLMGNLGLILVVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN
 KVISFLGCVAVQVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVMSPRVYVPLINASYVAGI
 LHATIHVATFSLFCGANEIRRVFCIPPLAISYSDHTNQLLLFYFVGSIELVTILIVLISYGLIL
 LAILKMYSAEGRRKVFSTCGAHLTGVSIIYGTILFMYVRPSSSYASDHDMIVSIFYTIVIPLLNPV
 IYSLRNKDVKDSMKKMFQKNQVINKVYFHTKK (SEQ ID NO: 127)

ATGTCGTACAGTATATACAAGAGCACAGTTAACATCCCCCTTGAGTCATGGTGTTGTTTCATT
 CTTTTTGTCAATAATGAAGTGAACCTTTATGCATATCTTCAAGTTTGTTCTAGATTTC AAC
 ATGAAGAATGTCAGTGAAGTTACCTTATTTGTACTGAAGGGCTTCACAGACAATCTTGAAC
 TGCAGACTATCTTCTTCTTCTCCTGTTTCTAGCAATCTACCTCTTCACTCTCATGGGAAATTA
 30 GGACTGATTTAGTGGTCATTAGGGATTCCAGCTCCACAAACCCATGTACTATTTCTGA
 GTATGTTGCTTCTGTGGATGCCTGCTATTCCCTCAGTTATTACCCCAAATATGTTAGTAGAT
 TTTACGACAAAGAATAAAGTCATTTTATTCCTTGATGTGTAGCACAGGTGTTTCTTGCTT
 GTAGTTTTGGAACACAGAATGCTTTCTCTTGCTGCAATGGCTTATGATCGCTATGTAGC
 CATCTACAACCTCTCCTGTATTGAGTGCATGTCACCCAGAGTCTACATGCCACTCATC
 35 AATGCTTCCTATGTTGCTGGCATTTCATGCTACTATACATACAGTGGCTACATTTAGCCT
 ATCCTTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTTGATATCCCTCCTCTCCTTGCTA
 TTTCTTATTCTGACACTCACACAAACCAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG
 CTGGTCACTATCCTGATTGTTCTGATCTCCTATGGTTTGATTCTGTTGGCCATTCTGAAGAT
 GTATTCTGCTGAAGGGAGGAGAAAAGTCTTCTCCACATGTGGAGCTCACCTAACTGGAGT
 40 GTCAATTTATTATGGGACAATCCTCTTCATGTATGTGAGACCAAGTCCAGCTATGCTTCG
 GACCATGACATGATAGTGTCAATATTTTACACCATTGTGATTCCCTTGCTGAATCCCGTCAT
 CTACAGTTTGAGGAACAAAGATGTAAAAGACTCAATGAAAAAAATGTTTGGGAAAAATCA
 GGTTATCAATAAAGTATATTTTCACTAAAAAATAA (SEQ ID NO: 128)

AOLFR70 sequences:

MDSTFTGYNLYNLQVKTEMDKLSSGLDIYRNPLKNKTEVTMFILTGFTDDFELQVFLFLFFAI
 YLFTLIGNLGLVVLVIEDSWLHNPMPYYFLSVLSFLDACYSTVVTPKMLVNFLAKNKSISFIGCA
 TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVMSPRVYVPLITASYVAGILHATIHIVA
 TFSLSFCGSNEIRHVFCMPPLAISCSHTNQLLLFYFVGSIEIVTILIVLISCDFILLSILKMHS
 50 KGRQKAFSTCGSHLTGVTIYHGTLVSYMRPSSSYASDHDIIVSIFYTIVIPKLNPIIYSLRNKEVK
 KAVKKMLKL VYK (SEQ ID NO: 129)

ATGGACTCCACTTTCACAGGCTATAACCTTTATAACCTGCAAGTAAAAAAGTGAATGGACA
 AGTTGTGTCAGGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAGTCACCA
 55 TGTTTATATTGACAGGCTTCACAGATGATTTTGAGCTGCAAGTCTTCCTATTTTACTATTT
 TTTGCAATCTATCTCTTACCTTGATAGGCAATTTAGGGCTGGTTGTGTTGGTCATTGAGG

ATTCCTGGCTCCACAACCCCATGTATTATTTTCTTAGTGTTTTATCATTCTTGGATGCTTGC
TATTCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCTGGCAAAAAATAAATCCATTT
CATTTATCGGATGTGCAACACAGATGCTTCTTTTGTACTTTTGGAACTACAGAATGTTTT
CTCTTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCCTCTCCTGTATTCACT
5 GAGCATGTACCCAGAGTCTATGTGCCACTCATCACTGCTTCCTACGTTGCTGGCATTITAC
ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCCTTCTGTGGATCCAATGAAATTAG
GCATGTCTTTTGTGATATGCCTCCTCTCCTTGCTATTTCTTGTCTGACACTCACACAAACC
AGCTTCTACTCTTCTACTTTGTGGGTTCTATTGAGATAGTCACTATCCTGATTGTCCTCATT
TCCTGTGATTTCACTTCTGTTGTCCATTCTGAAGATGCATTCTGCTAAGGGAAGGCAAAAGG
10 CCTTCTCTACATGTGGCTCTCACCTAACTGGAGTGACAATTTATCATGGAACAATTCTCGTC
AGTTATATGAGACCAAGTTCAGCTATGCTTCAGACCATGACATCATAGTGTCAATATTTT
ACACAATTGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAAA
AAAGGCAGTGAAGAAAATGTTGAAATTGGTTTACAAATGA (SEQ ID NO: 130)

15 **AOLFR71 sequences:**

MGRNNTNVPDFIL TGLSDSEEVQMALFILFLLIYLITMLGNVGMILIIRLDLQLHTPMYFFLTH
LSFIDLSYSTVITPKTLANLLTSNYISFMGCFAQMFFFVFLGAAECFLSSMAYDRYVAICSPRLY
PVIMSKRLCCALVTGPYVISFINSFVNVVWMSRLHFCDSNVVRHFFCDTSPILALSCMDTYDIEI
MIHILAGSTLMVSLJTISASYVSILTKINSTSGKQKALSTCASHLLGVTIFYGTMIFTYLPKPK
20 SYSLGRDQVASVFTYVIPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

ATGGGTAGAAGAAATAACACAAATGTGCCTGACTTCATCCTTACGGGACTGTCAGATTCTG
AAGAGGTCCAGATGGCCCTCTTTATACTATTTCTCCTGATATACCTAATTACTATGCTGGGC
AATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATTGATTTTT
25 TCCTTACTCACTTGTCATTTATTGACCTCAGTTACTCAACTGTCATCACACCTAAAACCTTA
GCGAACTTACTGACTTCCAATATATTTCTTCTCATGGGCTGCTTTGCCCAGATGTTCTTTTT
TGTCTTCTTGGGAGCTGCTGAATGTTTTCTTCTCTCATCAATGGCCTATGATCGCTACGTAG
CTATCTGCAGTCTCTACGTTACCCAGTTATTATGTCCAAAAGGCTGTGTTGCGCTCTTGTC
ACTGGGCCCTATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC
30 TGCATTTCTGCGACTCAAATGTAGTTCGTCACTTTTCTGCGACACGTCCTCAATTTTAGCT
CTGTCCTGCATGGACACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCCACCC
TGATGGTGTCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCTGAAA
ATTAATTCCACTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCCTCTCATCTCTTGGGAG
TCACCATCTTTTATGGAACATGATTTTTACTTATTTAAAACCAAGAAAGTCTTATTCTTTG
35 GGAAGGGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCATGCTGAATCCACTCAT
TTATAGTCTTAGAAACAAAGAAGTTAAAAATGCTCTCATTAGAGTCATGCAGAGAAGACA
GGACTCCAGGTAA (SEQ ID NO: 132)

40 **AOLFR72 sequences:**

MAPENFTRVTEFILTGVSSCPQLIPLFLVFLVLYGLTMAGNLGIITLTSVDSRLQTPMYFFLQHL
ALINLGNSTVIAPKMLINFLVKKKTTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL
YMVVSRRLCLLVSLTYLYGFSTAIVSSYVFSVSYCSSNIINH FYCDNVPLLALSCSDTYLPE
TVVFISAATNVVGLIIVLVSYFNIVLSILKICSEGRKKAFTSCASHMMAVTIFYGTLLFMYVQP
45 RSNHSLDTHDDKMASVFTYVIPMLNPLIYSLRNKDVKTALQRFMTNLCYSFKTM (SEQ ID NO:
133)

ATGGCTCCTGAAAATTTACCCAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC
CAGAGCTCCAGATTCCCCTCTTCTGGTCTTTCTGGTGCTCTATGGGCTGACCATGGCAGG
GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT
50 TCCTGCAACATCTGGCTCTCATTAATCTTGGTAACTCTACTGTCAATTGCCCTAAAATGCTG
ATTAATTTTTAGTAAAGAAGAAACTACCTCATTCTATGAATGTGCCACCAACTGGGAG
GGTTCTTGTCTTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCCTGTGACCGCTAT
GTGGCTATTTGTAACCCTCTGCTGTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGCT
GGTCTCCCTCACATACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCATCTTATGTATTCT
55 CTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTTACTGTGATAATGTTCTCTGTTA
GCATTATCTTGTCTGATACTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA

ATGTGGTTGGTTCCTTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTTGTCTATTTTA
 AAAATATGTTTCATCAGAAGGAAGGAAAAAGCCTTTTCTACCTGTGCTTCACATATGATGG
 CAGTCACAATTTTTTATGGGACATTGCTATTTCATGTATGTGCAGCCCCGAAGTAACCATTC
 ATTGGATACTGATGATAAGATGGCTTCTGTGTTTTACACGTTGGTAATTCCTATGCTGAAT
 5 CCCTTGATCTACAGCCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTCATGACA
 AATCTGTGCTATTCTTTAAACAATGTAA (SEQ ID NO: 134)

AOLFR73 sequences:

MNHVVKHNHTAVTKVTEFILMGITDNPLQAPLFGFLFIYLVTVIGNLGMVILTYLDSKLHTP
 10 MYFFLRHLSITDLGYSTVIAPKMLVNFIVHKNTISYNWYATQLAFFEIFIHSELFILSAMAYDRYV
 AICKPLLVIHMAEKVLWVLVIVPYLYSTFVSFLFTIKLFKLSFCGSNIISYFYCDCIPLMSILCSDT
 NELELILIFSGCNLLFSLSIVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVVIMFYGTLLFIYL
 QPKSSHTLAIDKMASVFYTLIPMLNPLIYSLRNKEVKDALKRTLNRFKIPI (SEQ ID NO: 135)

ATGAATCATGTGGTAAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTCTCA
 TGGGGATTACAGACAACCCTGGGCTGCAGGCTCCACTGTTGGACTCTTCCTCATCATATA
 TCTGGTCACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGCTA
 CACACCCCCATGTACTTTTTCTTAGACATTTGTCAATCACTGATCTTGGTTACTCCACTGT
 CATTGCCCCGAAGATGTTAGTAAACTTCATAGTGCACAAAAACACAATTTCTTACAATTGG
 20 TATGCCACTCAGCTAGCATTCTTTGAGATTTTCATCATCTCTGAGCTCTTTATTCTATCAGC
 AATGGCCTATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGTACGTGATCATCATGGCA
 GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTCTATAGCACGTTTGTGTCACTATT
 TCTCACAATTAAGTTATTTAACTGTCCTTCTGTGGCTCAAACATAATCAGCTATTTTTACT
 GTGACTGTATCCCTCTGATGTCCATACTCTGTTCTGACACAAATGAATTAGAATTAATAAT
 25 TTTGATCTTCTCAGGCTGTAATTTGCTCTTCTCCCTCTCAATTGTTCTCATATCCTACATGTT
 TATTCTAGTGGCCATTCTCAGAATGAAGTCAAGGAAAGGGAGGTACAAAGCCTTCTCCACC
 TGTAGCTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTATTTATTTACTTGCA
 ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTTATACCCTGTTG
 ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAAGATGCTCTAA
 30 AGAGAACTTTAACCAATCGATTCAAAATTTCCATTAA (SEQ ID NO: 136)

AOLFR74 sequences:

MEQHNLTTVNEFILTGITDIAELQAPLFAFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH
 35 LAFMDLGYSTTVGPKMLVNFVVDKNIISYFCATQLAFFLVFIGSELFILSAMSVDLYVAICNPL
 LYTVIMSRRVCQVLVAIPYLYCTFISLLVTIKIFTLSCGYNVISHFYCDSLPLPLLCNSNTHEIELI
 ILIFAAIDLISLLIVLLSYLLILVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLLFMYVQPKSSH
 SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLCNIFV (SEQ ID NO: 137)

ATGGAACAACACAATCTAACAACGGTGAATGAATTCATTCTTACGGGAATCACAGATATC
 40 GCTGAGCTGCAGGCACCATTATTTGCATTGTTCCCTCATGATCTATGTGATCTCAGTGATGG
 GCAATTTGGGCATGATTGTCCTACCAAGTTGGACTCCAGGTTGCAACCCCTATGTACTT
 TTTTCTCAGACATCTGGCTTTTCATGGATCTTGGTTATTCAACAACCTGTGGGACCCAAAATG
 TTAGTAAATTTGTTGTGGATAAGAATATAATTTCTTATTATTTTTGTGCAACACAGCTAGC
 TTTCTTTCTTGTGTTTCATTGGTAGTGAACTTTTTATTCTCTCAGCCATGTCCTACGACCTCT
 45 ATGTGGCCATCTGTAACCTCTGCTATACACAGTAATCATGTGCAGGAAGGGTATGTCAGGT
 GCTGGTAGCAATCCCTTACCTCTATTGCACATTCAATTTCTTCTAGTCACCATAAAGATTT
 TTACTTTATCCTTCTGTGGCTACAACGTCATTAGTCATTTCTACTGTGACAGTCTCCCTTTG
 TTACCTTTGCTTTGTTCAAATACACATGAAATTGAATTGATAATTCTGATCTTTTGACGTAT
 TGATTTGATTCATCTCTCTGATAGTCTTTTATCTTACCTGCTCATCCTTGTAGCCATTCT
 50 CAGGATGAATTCTGCTGGCAGACAAAAGGCTTTTTCTACCTGTGGAGCCCACCTGACAGTG
 GTCATAGTGTCTATGGGACTTTGCTTTTCATGTACGTGCAGCCCAAGTCCAGTCATTCCTT
 TGACACTGATAAAGTGGCTTCCATATTTTACACCCTGGTTATCCCCATGTTGAATCCCTTGA
 TCTATAGTTTACGAAACAAAGATGTAAAATATGCCCTACGAAGGACATGGAATAACTTATG
 TAATATTTTTGTTTAA (SEQ ID NO: 138)

AOLFR75 sequences:

MEGKNQTNISEFLLGFSSWQQQVLLFALFLCLYLTGLFGNLLILLAIGSDHCLHTPMYFFLA
 NLSLVDLCLPSATVPKMLLNIQTQTQISYPGCLAQMYFCMMFANMDNFLTVMAYDRYVAI
 CHPLHYSTIMALRLCASLVAAPWVIAILNPLLHTLMMAHLHFCSDNVIHHFFCDINSLPLSCSD
 5 TSLNQLSVLATVGLIFVVPVCILVSYILIVSAVMKVPSAQGKLKAFSTCGSHLALVILFYGANT
 GVYMSPLSNHSTEKDSAASVIFMVVAPVLNPFIFYSLRNNELKGTLLKTLRPGAVAHACNPSTL
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)

ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTTCTCCTCCTGGGCTTCTCAAGTTGGC
 10 AACACAGCAGGTGCTACTCTTTGCACTTTTCCTGTGTCTCTATTTAACAGGGCTGTTTGGA
 AACTTACTCATCTTGCTGGCCATTGGCTCGGATCACTGCCTTCACACACCCATGTATTTCTT
 CCTTGCCAATCTGTCCTTGGTAGACCTCTGCCTTCCCTCAGCCACAGTCCCCAAGATGCTAC
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCCTGGCTCAGATGTATTT
 CTGTATGATGTTTGCCAATATGGACAATTTTCTTCTCACAGTGATGGCATATGACCGTTAC
 15 GTGGCCATCTGTCACCCCTTTACATTACTCCACCATTATGGCCCTGCGCCTCTGTGCCTCTCT
 GGTAGCTGCACCTTGGGTCATTGCCATTTTGAACCCTCTCTTGACACTCTTATGATGGCCC
 ATCTGCACTTCTGCTCTGATAATGTTATCCACCATTCTTCTGTGATATCAACTCTCTCCTC
 CCTCTGTCCTGTTCCGACACCAGTCTTAATCAGTTGAGTGTTCTGGCTACGGTGGGGCTGA
 TCTTTGTGGTACCTTCAGTGTGTATCCTGGTATCCTATATCCTCATTGTTTCTGCTGTGATG
 20 AAAGTCCCTTCTGCCCCAAGGAAAACCTCAAGGCTTTCTCTACCTGTGGATCTCACCTTGCCCT
 GGTCACTTCTTTCTATGGAGCAAACACAGGGGTCTATATGAGCCCCCTTATCCAATCACTCT
 ACTGAAAAAGACTCAGCCGCATCAGTCATTTTATGGTTGTAGCACCTGTGTTGAATCCAT
 TCATTTACAGTTTAAGAAACAATGAACTGAAGGGGACTTTAAAAAAGACCCTAAGCCGCGC
 CGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA
 25 TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)

AOLFR76 sequences:

MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLITLTGNLGMILILLDSHLHTPMYFFLSNLSLA
 GIGYSSAVTPKVLGTGLIEDKAISYSACAAQMFFCAVFATVENYLLSSMAYDRYAAVCNPLHY
 30 TTTMTTRVCACLAIGCYVIGFLNASIQIGDTFRLSFCMSNVIIHHFFCDKPAVITLTCSEKHISELIL
 VLISSFNVFALLVTLISYLFILITILKRHTGKGYYQKPLSTCGSHLIAIFLYITVIIMYIRPSSSHSM
 DTDKIASVFYTMIPMLSPIVYTLRNKDVKNFAFMKVVEKAKYSLDSVF (SEQ ID NO: 141)

ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCCAGAA
 35 CTACAGTTCCCCTCTTTATCATGTTTACCCTCATCTACCTCATCACTCTGACTGGGAACCT
 GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTTCTCA
 GTAACCTGTCTCTTGCAGGCATTGGTTACTCCTCAGCTGTCACTCCAAAGGTTTTAACTGG
 GTTGCTTATAGAAGACAAAGCCATCTCCTACAGTGCCTGTGCTGCTCAGATGTTCTTTTGT
 GCAGTCTTTGCCACTGTGAAAAATTACCTCTTGCTCCTCAATGGCCTATGACCGCTACGCAG
 40 CAGTGTGTAACCCCTACATTATACCACCACCATGACAACACGTGTGTGTGCTTGTCTGGC
 TATAGGCTGTTATGTCATTGGTTTTCTGAATGCTTCTATCCAAATTGGAGATACATTCGCC
 TCTCTTTCTGCATGTCCAATGTGATTCACTTTTTCTGTGACAAACCAGCAGTCATTACT
 CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTTGTTCTTATATCAAGTTTTAATGT
 CTTTTTGCACCTCTTGTTACCTTGATTTCCTATCTGTTTCATATTGATCACCATTCTTAAGAG
 45 GCACACAGGTAAGGGATACCAGAAGCCTTTATCTACCTGTGGTTCTCACCTCATTGCCATT
 TTCTTATTTTATATAACTGTCATCATCATGACATACGACCAAGTTCCAGTCATTCCATGGA
 CACAGACAAAATTGCATCTGTGTTCTACACTATGATCATCCCCATGCTCAGTCCTATAGTCT
 ATACCCTGAGGAACAAAGACGTGAAGAATGCATTCATGAAGGTTGTTGAGAAGGCAAAAT
 ATTCTCTAGATTCAGTCTTTTAA (SEQ ID NO: 142)

50

AOLFR77 sequences:

MGDVNQSVASDFILVGLFSHSGSRQLLFSLVAVMFVIGLLGNTVLLFLIRVDSRLHTPMYFLLS
 QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFFLTLMGVAEGVLLVLSYDRYVAVC
 QPLQYPVLMRRQVCLLMGSSWVGVNLASIQTSITLHFPYCASRVDHFFCEVPALLKLSCA
 55 DTCAYEMALSTSGVLILMLPLSLIATSYGHVLQAVLSMRSEEARHKAVTTCSSHITVVGLFYGA

AVFMYMVP CAYHSPQQDNVVS LFYSLVTP TNLNPLIYSLRNPEVWMALVKVLSRAGLRQMC
(SEQ ID NO: 143)

5 ATGGGGGATGTGAATCAGTCGGTGGCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACT
CAGGATCACGCCAGCTCCTCTCTCCCTGGTGGCTGTCATGTTTGTATAGGCCTTCTGGGC
AACACCGTTCTTCTCTTCTTGATCCGTGTGGACTCCCGGCTCCACACACCCATGTACTTCCT
GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCACCATCCCCAAGATGGCA
TCAGACTTTCTGCGGGGAGAAGGTGCCACCTCCTATGGAGGTGGTGCAGCTCAAATATTCT
10 TCCTCACACTGATGGGTGTGGCTGAGGGCGTCCTGTTGGTCCTCATGTCTTATGACCGTTA
TGTTGCTGTGTGCCAGCCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGCTG
ATGATGGGCTCCTCCTGGGTGGTAGGTGTGCTCAACGCCTCCATCCAGACCTCCATCACCC
TGCAATTTTCCCTACTGTGCCTCCCGTATTGTGGATCACTTCTTCTGTGAGGTGCCAGCCCTA
CTGAAGCTCTCCTGTGCAGATACCTGTGCCTACGAGATGGCGCTGTCCACCTCAGGGGTGC
TGATCCTAATGCTCCCTCTTTCCCTCATCGCCACCTCCTACGGCCACGTGTTGCAGGCTGTT
15 CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGCTGTCACCACCTGCTCCTCGCACATCA
CGGTAGTGGGGCTCTTTTATGGTGGCGCCGTGTTTCATGTACATGGTGCCTTGCAGCTACCA
CAGTCCACAGGATAACGTGGTTTCCCTCTTCTATAGCCTTGTACCCCTACACTCAAC
CCCTTATCTACAGTCTGAGGAATCCGGAGGTGTGGATGGCTTGGTCAAAGTGCTTAGCA
GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

20 **AOLFR78 sequences:**

MSPDGNHSSDPTEFVLAGLPNLNSARVELFSVFLVYLLNL TGNVLIVGVVRADTRLQTPMYF
FLGNLSCLEILLTSVIIPKMLSNFLSRQHTISFAACITQFYFYFFLGASEFLLAVMSADRYLAICH
PLRYPLMSGAVCFRVALACWVGGGLVPVLGPTVAVALLPFCCKQGAVVQHFFCDSGPLRLAC
25 TNKKLEETDFVLASLVIVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVVTLFYGSAI
FLYVRPSQSGSVDTNWAVTVITTFVTPLLPFIYALRNEQVKEALKDMFRKVAVGLGNLLD
KCLSEKAVK (SEQ ID NO: 145)

30 ATGAGTCTGATGGGAACACAGTAGTGATCCAACAGAGTTCGTCCTGGCAGGGCTCCCA
AATCTCAACAGCGCAAGAGTGGAATTATTTCTGTGTTTCTTCTTGTCTATCTCCTGAATCT
GACAGGCAATGTGTTGATTGTGGGGGTGGTAAGGGCTGATACTCGACTACAGACCCCTAT
GTACTTCTTTCTGGGTAACCTGTCTGCCTAGAGATACTGCTCACTTCTGTATCATTTCCAA
AGATGCTGAGCAATTTCTCTCAAGGCAACACACTATTTCTTTGCTGCATGTATCACCCA
ATTCTATTTCTACTTCTTTCTCGGGGCTCCGAGTTCCTTACTGTTGGCTGTCTGTGCGG
35 ATCGCTACCTGGCCATCTGTATCCTCTGCGCTACCCCTTGCTCATGAGTGGGGCTGTGTG
CTTTCGTGTGGCCTTGGCCTGCTGGGTGGGGGGACTCGTCCCTGTGCTTGGTCCACAGTG
GCTGTGGCCTTGCTTCTTTCTGTAAGCAGGGTGCTGTGGTACAGCACTTCTTCTGCGACA
GTGGCCCACTGCTCCGCCTGGCTTGCACCAACACCAAGAAGCTGGAGGAGACTGACTTTGT
CCTGGCCTCCCTCGTCATTGTATCTTCTTGCTGATCACTGCTGTGTCTACGGCCTCATTG
40 TGCTGGCAGTCTGAGCATCCCTCTGCTTCAGGCCGTGAGAAGGCCCTTCTTACCTGTAC
CTCCCACTTGATAGTGGTGACCTCTTCTATGGAAGTGCCATTTTCTCTATGTGCGGCCAT
CGCAGAGTGTTCTGTGGACACTAACTGGGCAGTGACAGTAATAACGACATTTGTGACAC
CACTGTTGAATCCATTCTATGCCTTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA
CATGTTTAGGAAGGTAGTGGCAGGCGTTTATAGGGAATCTTTACTTGATAAATGTCTCAGT
45 GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

AOLFR79 sequences:

MTPGELALASGNHTPVTKFILQGFNSYPDLQELLFGAILLIYAITVVGNLGMMLIFTDSHLQSP
MYFFLNVL SFLDICYSVVT PKLLVNFLVSDKSISFEGCVVQLAFFVHVTAESFLLASMA YDR
50 FLAICQPLHYGSIMTRGTCLQLVAVSYAFGGANS AIQTGNVFALPFCGPNQLTHYYCDIPPLH
LACANTATARVVLVYFVSALVTLLPAAVILTSYCLVLVAIGRMRSVAGREKDLSTCASHFLAIAI
FYGTVVFTYVQPHGSTNNTNGQVVSFYTHIIPMLNPFYISLRNKEVK GALQRKLQVNI FPG
(SEQ ID NO: 147)

55 ATGACACCTGGAGAACTAGCCCTTGCCAGTGGCAACCAACACCCCAAGTTCATCT
TGCAGGGATTCTCCAATTATCCAGACCTCCAGGAGCTTCTCTTCGGAGCCATCCTGCTCAT

CTATGCCATAACAGTGGTGGGCAACTTGGGAATGATGGCACTCATCTTCACAGACTCCCAT
CTCCAAAGCCCAATGTATTTCTTCCTCAATGTCCTCTCGTTTCTTGATATTTGTTACTCTTCT
GTGGTCACACCTAAGCTCTTGGTCAACTTCCTGGTCTCTGACAAGTCCATCTCTTTTGAGG
GCTGTGTGGTCCAGCTCGCCTTCTTTGTAGTGCATGTGACAGCTGAGAGCTTCTGTCTGGC
5 CTCCATGGCCTATGACCGCTTCCTAGCCATCTGTCAACCCCTCCATTATGGTCTATCATGA
CCAGGGGGACCTGTCTCCAGCTGGTAGCTGTGTCTATGCATTTGGTGGAGCCAACTCCGC
TATCCAGACTGGAAATGTCTTTGCCCTGCCTTTCTGTGGGCCCCAACAGCTAACACACTAC
TACTGTGACATAACACCCCTTCTCCACCTGGCTTGTGCCAACACAGCCACAGCAAGAGTGG
TCCTCTATGTCTTTTCTGCTCTGGTCAACCTTCTGCTGCTGCAGTCATTCTCACCTCCTACT
10 GCTTGGTCTTGGTGGCCATTGGGAGGATGCGCTCAGTAGCAGGGAGGGAGAAGGACCTCT
CCACTTGTGCTTCCACTTTCTGGCCATTGCCATTTTCTATGGCACTGTGGTTTTCACCTAT
GTTTCAGCCCCATGGATCTACTAACAATACCAATGGCCAAGTAGTGTCCGTCTTCTACACCA
TCATAATTCCCATGCTCAATCCCTTCATCTATAGCCTCCGCAACAAGGAGGTGAAGGGCGC
TCTGCAGAGGAAGCTTCAGGTCAACATCTTTCCCGGCTGA (SEQ ID NO: 148)

15

AOLFR80 sequences:

MEGINKTAKMQFFRPFPSPDPEVQMLIFVVFLLMMYLTSLGGNATIAVIVQINHSLHTPMYFFLA
NLAVLEIFYTSSITPLALANLLSMGKTPVSITGCGTQMFFVFLGGADCVLLVVMAYDRFIAICH
PLRYRLIMSWSLCVELLVGSLVLGFLSLPLTILFHLFPCHNDEIYHFYCDMPAVMRLACADTR
20 VHKTALYIISFIVLSIPLSLISYVFIVVAILRIRSAEGRQQAYSTCSSHILVLLQYGCTSFYILSPS
SSYPEMGRVVSVAYTFITPILNPLIYSLRNKELKDALKALRF (SEQ ID NO: 149)

ATGGAAGGAATAAATAAAACTGCAAAGATGCAGTTTTTCTTTCTGTCATTCTCACCTGACC
CTGAGGTCCAGATGCTGATTTTGTGGTCTTCCTGATGATGTATCTGACCAGCTCGGTGG
25 AAATGCTACAATGCAGTCATTGTTTCAGATCAATCATTCCCTCCACACCCCCATGTACTTTT
TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCCATCACCCCCATTGGCCTTG
GCAAACCTCCTTTCAATGGGCAAACTCCTGTTTCCATCACGGGATGTGGCACCCAGATGT
TTTTCTTTGTCTTCTTGGGTGGGGCTGATTGTGTCTGCTGGTAGTCATGGCTTATGACCGG
TTTATAGCGATCTGTCACCCTCTGCGATACAGGCTCATCATGAGCTGGTCTTGTGTGTGG
30 AGCTGCTGGTAGGCTCCTTGGTGTGGGGTTCCTGTTGTCACTGCCACTCACCATTTAATC
TTCCATCTCCCATCTGCCACAATGATGAGATCTACCACTTCTACTGTGACATGCCTGCAGT
CATGCGCCTGGCTTGTGCAGACACACGCGTTCACAAGACTGCTCTGTATATCATCAGCTTC
ATCGTCCTTAGCATCCCCCTCTCATTGATCTCCATCTCCTATGTCTTCATCGTGGTAGCCAT
TTTACGGATCCGGTCAGCAGAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC
35 TTAGTGGTCTCCTGCAGTATGGCTGCACCAGCTTTATATACTTGTCCTCCCATTTTAAAC
CTCTCCTGAGATGGGCCGGGTGGTATCTGTGGCCTACACATTTATCACTCCCATTTTAAAC
CCCTTGATCTATAGTTTGAGGAACAAGGAACTGAAAGATGCCCTAAGGAAAGCATTGAGA
AAATTCTAG (SEQ ID NO: 150)

AOLFR81 sequences:

MGVKNHSTVTEFLLSGLTEQAELQLPLFLFLGIYTVTVVGNLSMISIIRLNRLHTPMYFFLSS
LSFLDFCYSSVITPKMMKLWMESHLIVPETRPSRMSNQTLVTEFILQGFSEHPEYRVFLFSCF
LFLYSGALTGNVLITLAITFNPGLHAPMYFFLLNLATMDIICTSSIMPKALASLVSEESSISYGGC
MAQLYFLTWAASSELLLLTVMAYDRYAACHPLHYSSMMSKVFCGLATAVWLLCAVNTAIH
45 TGLMLRLDFCGPNVHHFFCEVPPLLLLSSTYVNGVMIVLADAFYGIVNFMNTIASYGIVSSI
LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL
IYTLRNKEVKAALRKLFPFFRN (SEQ ID NO: 151)

ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCAGAAACCCGTCCAGCCCAAGGATG
50 ATGAGTAACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTCGGAGACCCAGAAT
ACCGGGTGTTCTTATTACAGCTTTTCTCTCTCTACTCTGGGGCCCTCACAGGTAATGTC
CTCATGCTTGGCCATCAGTTCAACCTGGGCTCCACGCTCCTATGTACTTTTCTTACT
CAACTTGGCTACTATGGACATTATCTGCACCTCTTCCATCATGCCCAAGGCGCTGGCCAGT
CTGGTGTGGAAGAGAGCTCCATCTCCTACGGGGGCTGCATGGCCAGCTCTATTTCTCA
55 CGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTTCATGGCCTATGACCGGTACGCAGC
CATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC

ACAGCCGTGTGGCTGCTCTGCGCCGTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT
TGGATTTCTGTGGCCCAATGTCATTATCCATTTCTTCTGCGAGGTCCCTCCCCTGCTGCTT
CTCTCCTGCAGCTCCACCTACGTCAACGGTGTGATGATTGTCCTGGCGGATGCTTTCTACG
GCATAGTGAACCTTCTGATGACCATCGCGTCTATGGCTTCATCGTCTCCAGCATCCTGAA
5 GGTGAAGACTGCCTGGGGGAGGCAGAAAGCCTTCTCCACCTGCTCTTCCCACCTACCGTG
GTGTGCATGTATTACACCGCTGTCTTCTACGCCTACATAAGCCCGGTCTCTGGCTACAGCG
CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACTGTGCTGAGTCCTACCCTCAACCCCT
CATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTCCCTTTCTTC
AGAAATTAA (SEQ ID NO: 152)

10

AOLFR82 sequences:

MQLNNNVTEFILLGLTQDPFWKKIVFVIFLRLYLGTLLGNLLIIISVKASQALKNPMFFFLFYLSL
SDTCLSTSIAPRMIVDALLKKTISFSECMIQVFSSHVFGCLEIFILITAVDRYVDICKPLHYMTII
SQWVCGVLMVAWVWGSCVHSLVQIFLALSLPFCGPNVINHCFCDLQPLLKQACSETYVNNLL
15 VNSGAICAVSYVMLIFSIVIFLHSLRNHSAEVIKKALSTCVSHIIVILFFGPCIFMYTCPATVFP
MDKMIAVFYTVGTSFLNPVIYTLKNTVEKVSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGGATTGACACAGGATCCTTTTT
GGAAGAAAATAGTGTTTGTATTTTTTTGCCTCTCTACTTGGGAACACTGTTGGGTAATTT
20 GCTAATCATTATTAGTGTCAAGGCCAGCCAGGCACTTAAGAACCCAATGTTCTTCTTCTCTT
TTCTACTTATCTTTATCTGATACTTGCCCTCTCTACTTCCATAGCCCCTAGAATGATTGTGGA
TGCCCTTTTGAAGAAGACAACATATCTCCTTCAGCGAGTGCATGATCCAAGTCTTTTCATCC
CATGTCTTTGGCTGCCTGGAGATCTTCATCCTCATCCTCACGGCTGTTGACCGCTATGTGGA
CATCTGTAAGCCCTGCACTACATGACCATCATAAGCCAGTGGGTCTGTGGTGTGTTTGATG
25 GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAGATTTTTCTTGCCCTGAGTTT
GCCATTCTGTGGCCCCAATGTGATCAATCACTGTTTCTGTGACTTGCAGCCCTTGTGAAA
CAAGCCTGTTCAAGAACCTATGTGGTTAACCTACTCCTGGTTTCCAATAGTGGGGCCATTT
GTGCAGTGAGTTATGTATGCTAATAATTCTCCTATGTCATCTTCTTGCACTTCTTGAGAAAC
CACAGTGCTGAAGTGATAAAGAAAGCACTTCCACATGTGTCTCCCACATCATTGTGGTCA
30 TCTTGTTCTTTGGACCTTGCATATTTATGTACACATGCCCTGCAACCGTATTCCTCATGGAT
AAGATGATAGCTGTATTTTATACAGTTGGAACATCTTTTCTCAACCCTGTGATTTACACGCT
GAAGAATACAGAAGTGAAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATTGATCACAGA
TGACAAAAGATAA (SEQ ID NO: 154)

AOLFR83 sequences:

MGNWTAAVTEFVLLGFSLSREVELLLLVLPTFLLTLLGNLLIISTVLSCSRLHTPMYFFLCNL
SILDILFTSVISPKVLANLGRDKTISFAGCITQCYFYFFLGTVEFLLLTVMSYDRYATICPLRYT
TIMRPSVCIGTVVFSWVGFLSVLFPTILISQLPFCGSNIINHFFCDSGPLLALACADTTAIELMDF
MLSSMVILCCIVLVAYSITYIILTIVRIPSASGRKKAFNTCASHLTIVIPSGITVFIYVTPSQKEYL
40 EINKIPLVLSSVTPFLNPFYTLRNDTVQGVLRDVWVRVGRGVFEKRMRAVLRSLSSNKDHQ
GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

ATGGGTAAGTGGACTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCCTGAGCAGGG
AGGTGGAGCTGCTGCTCCTGGTGCTCCTGCTGCCACGTTCCTGCTGACTCTTCTGGGGAA
45 CCTGCTCATCATCTCCACTGTGCTGTCCTGCTCCCGCCTCCACACCCCATGTACTTCTTCT
TGTGCAACCTCTCTATCCTGGACATCCTCTTACCTCAGTCATCTCTCCAAAAGTGTGGCC
AACTTAGGATCTAGGGATAAAACCATCTCCTTTGCCGGATGTATCACCCAGTGCTATTTCT
ACTTTTTCTTGGGCACAGTTGAGTTCCCTCCTGCTGACGGTCATGTCCTATGACCGTTATGCC
ACCATCTGCTGCCCCCTGCGGTACACCACCATCATGAGACCTTCTGTCTGCATTGGGACCG
50 TTGTAATCTCTTGGGTGGGAGGCTTCTGTCTGTGCTCTTTCCAACCATCCTCATCTCCAG
CTGCCCTTCTGTGGCTCCAATATCATTAACCACTTCTTCTGTGACAGTGAGCCCTTGCTGGC
CCTGGCCTGTGTCAGACACCACTGCCATCGAGCTGATGGATTTTATGCTTTCTTCCATGGTC
ATCCTCTGCTGCATAGTCTCGTGGCCTATTCTATACGTACATCATCTTGACCATAGTGCG
CATTCCTTCTGCAAGTGGAAGGAAGAAGGCCTTTAATACCTGTGCTTCCCACCTGACCATA
55 GTCATCATTCCTAGTGGCATCACTGTGTTTATCTATGTGACTCCCTCCCAGAAAGAATATCT
GGAGATCAACAAGATCCCTTTGGTTCTGAGCAGTGTGGTGACTCCATTCTCAACCCCTTT

ATATATACTCTGAGGAATGACACAGTGCAGGGAGTCCTCAGGGATGTGTGGGTCAGGGTT
CGAGGAGTTTTTGAAGAGGATGAGGGCAGTGCTGAGAAGCAGATTATCCTCCAACAAA
GACCACCAAGGAAGGGCTTGCTCTTCTCCACCATGTGTCTATTCTGTAAAGCTCCAGTGTT
AG (SEQ ID NO: 156)

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AOLFR85 sequences:

MGAKNNVTEFVFLFGLFESREMQHTCFVVFVFLFHVLTVLGNLLVIITINARKTLKSPMYFFLSQL
SFADICYPSTTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY
TAIMDCRKCGLLAGASWLAGFLHSILQTLTVQLPFCGPNEIDNFFCDVHPLLKLACADTYMV
GLIVVANSGMISLASFFILISYVILLNLRSQSSDDRRAVSTCGSHVITVLLVLMPPMFMYIRPS
TTLAADKLIILFNIVMPPLNPLIYTLRNNDVKNAMRKLFRVKRSLGEK (SEQ ID NO: 157)

10

ATGGGTGCCAAGAACAATGTGACTGAGTTTGTGTTTTATTTGGCCTTTTTGAGAGCAGAGAGA
TGCAGCATACATGCTTTGTGGTATTCTTCCTCTTTCATGTGCTCACTGTCTGGGGAACCTT
CTGGTCATCATCACCATCAATGCTAGAAAGACCCTGAAGTCTCCCATGTATTTCTTCCTGA
GCCAGTTGTCTTTTGTGACATATGTTATCCATCCACTACCATAACCAAGATGATTGCTGAC
ACTTTTGTGGAGCATAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTCTGCCCA
CTTCTTTGGTGGCACTGAGATCTTCCTCCTTACAGCCATGGCCTATGACCGCTATGTGGCC
ATCTGTAGGGCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG
GGGCCCTCCTGGTTAGCTGGCTTCCTGCATTCCATCCTGCAGACCTCCTCACGGTTCAGCTG
CCTTTTTGTGGGCCCAATGAGATAGACAACCTTCTTCTGTGATGTTCACTCCCTGCTCAAGTT
GGCCTGTGCAGACACCTACATGGTAGGTCTCATCGTGGTGGCCAACAGCGGTATGATTTCT
TTAGCATCCTTTTTTATCCTTATCATTTCCTATGTTATCATCTTACTGAACCTAAGAAGCCA
GTCATCTGAGGACCGCGTAAGGCTGTCTCCACATGTGGCTCACACGTAATCACTGTCTCTT
TTGGTTCTCATGCCCCCATGTTCTATGTACATTCGTCCTCCCTCCACCACCCTGGCTGTGACAA
ACTTATCATCCTCTTTAAACATTGTGATGCCACCTTTGCTGAACCCTTTGATCTATACACTAA
GGAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG
AGAAGTGA (SEQ ID NO: 158)

20

25

AOLFR86 sequences:

MLVLLLMFLLVFIGNTAPAFSVTLESMDIPQNITEFFMLGLSQNSEVQRVLFVVFLLIYVVTVC
GNMLIVVTITSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFGAHE
LGGVEIILLTVMAYDRYVAICKPLHNTIMTRHLCAMLVGVAVWLGGFLHSLVQLLLVLWLPFC
GPNVINHFACDLYPLLEVACTNTYVIGLLVVANSGLICLLNFLMLAASYIVILYSLRSHSADGRC
KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMR
KLFTW (SEQ ID NO: 159)

35

ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT
CTCAGTGACCTTGGAATCTATGGACATACCACAAAATATCACAGAATTTTTCATGCTGGGG
CTCTCACAGAACTCAGAGGTACAGAGAGTTCTCTTGTGGTCTTTTGTGCTGATCTATGTGG
TCACGGTTTGTGGCAACATGCTCATTGTGGTCACTATCACCTCCAGCCCCACGCTGGCTTC
CCCTGTGATTTTTTCTGGCCAACCTATCCTTTATTGACACCTTTTATTCTTCTTCTATGGC
TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGCTGCATG
GCTCAGCTCTTTGGAGCTCATTTTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG
CTTATGACCGCTATGTGGCCATCTGTAAGCCCCTGCACAATACTACCATCATGACCAGGCA
TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGGCTTCCTGCATTCAATTGGTTTCA
CTCCTCCTGGTCTTTGGTTGCCCTTCTGTGGGGCCCAATGTGATCAATCACTTTGCCTGTGA
CTTGTACCTTTGCTGGAAGTTGCCTGCACCAATACGTATGTCAATTGGTCTGCTGGTGGTT
GCCAACAGTGGTTTAATCTGCCTGTTGAACTTCCTCATGCTGGCTGCCTCCTACATTGTCAT
CCTGTACTCCTTGAGGTCCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA
GCCCACTTCAATTGTTGTTGCCTTGTCTTTGTGCCCTGTATATTACTTATGTGCATCCATTT
TCTACTTTTACCTATAGACAAAAATATGGCATTATTTTATGGTATTCTGACACCTATGTTGAA
TCCACTCATTTATACCCTGAGAAATGAAGAGGTAAAAAATGCCATGAGAAAGCTCTTTACA
TGGTAA (SEQ ID NO: 160)

55

AOLFR87 sequences:

MNNIAQLSLGFDLGPISVLQKIILTKIILLFKMYVSNCPCAIHRKINYPNTKLDFEQVNNITEFI
LLGLTQNAEAQKLLFAVFTLIYFLTMVDNLIIIVTITTSFALDSPVYFFLSFFSFIDGCSSTMAP
KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEIILLVVMAYDCYVAICKPLYLITMNRQVCGL
5 LVAMAWVGGFLHALIQMLLIVWLPFCGPNVIDHFICDLFPLLKLSCTDTHVFGLFVAANSGLM
CMLIFSILITSYVLILCSQRKALSTCAFHITVVVLFVPCILVYLRPMITFPIDKAVSVFYTVVTPM
LNPLIYTLRNTEVKNAMKQLWSQIHWGNLDC (SEQ ID NO: 161)

10 ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTTAC
AGAAAATAATCCTGACCAAAATTATTTTATTGTTCAAAATGTATGTGTCAAATTGCAATCC
TTGTGCTATTACAGAAAAATCAATTATCCAAATACCAAACCTGGATTTCGAGCAAGTGAAC
AACATAACGGAATTCATCTTGCTTGGCCTGACACAGAACGCAGAGGCACAGAACTCTTGT
TTGCTGTGTTTACACTCATCTACTTTCTCACCATTGGTAGACAACCTAATCATTGTGGTGACA
15 ATCACCACCAGCCCAGCCCTGGACTCCCCCGTGTATTTTTTCTGTCTTTCTTTCTTTCAT
AGATGGCTGCTCCTCTTCTACCATGGCCCCCAAAATGATATTTGACTTACTCACTGAAAAG
AAAATATTTCTTTCAGTGGGTGCATGACCCAGCTCTTTGTAGAACATTTCTTTGGGGGAG
TTGAGATCATTCTGCTCGTGGTGATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCCT
GTACTACCTGATCACAAATGAACAGGCAGGTATGTGGCCTCCTGGTGGCCATGGCATGGGTC
20 GGGGGATTCTTCACGCTCTGATTCAAATGCTTTTAATAGTCTGGCTGCCCTTCTGTGGCCC
CAATGTCAATTGACCATTTTCTGTGACCTTTTCCCTCTGCTAAACTCTCCTGCCTGACA
CTCACGTCTTTGGACTCTTTGTTGCCGCCAACAGTGGGCTGATGTGTATGCTCATTTTTTCT
ATTCTTATTACCTCTTACGTCCTAATCCTCTGCTCACAGCGGAAGGCTCTCTTACCTGCGC
CTTCCATATCACTGTAGTCGTCCTATTCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA
25 TGATCACCTTCCCTATTGATAAAGCTGTGTCTGTGTTTTATACTGTGGTAACACCCATGTTA
AACCCTTTAATCTACACCCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG
AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

AOLFR88 sequences:

30 MWQKNQTSADFILEGLFDDSLTHLFLSLTMVVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ
LSLMDLMHVSTIILKMATNYLSGKKSISFVGCATQHFLYLCLGGAECFLLAVMSYDRYVAICH
PLRYAVLMNKKVGLMMAVMSWLGA SVNSLIHMAILMHFPFCGPRKVYHFYCEFPVVKLVC
GDITVYETTVYISSILLPIFLISTSYVFIQSVIQMRSSGSKRNAFATCGSHLTVVSLWFGACIFS
YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVAKALRRVLRRDVITQCIQRLQLWLP
RV (SEQ ID NO: 163)

35 ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGGCTCTTCGATGACT
CCCTTACCCACCTTTTCTTTCTCCTTGACCATGGTGGTCTTCCTTATTGCGGTGAGTGGC
AACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACACCAATGTATTTCT
40 GCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAATCATCCTGAAGATGGCT
ACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTCC
TCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCATGTCTATGACCGCTAT
GTTGCCATCTGTCTCATCCACTGCGCTATGCTGTGCTCATGAACAAGAAGGTGGGACTGATGA
TGGCTGTCTATGTCTGTTGGGGGCATCCGTGAACTCCCTAATTCACATGGCGATCTTGAT
45 GCACTTCCCTTTCTGTGGGCCCTCGGAAAGTCTACCACTTCTACTGTGAGTTCCCAGCTGTTG
TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTACATCAGCAGCATTCT
CCTCCTCCTCCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTTCAAAGTGTCAATCA
GATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCTCCACCTCACGGTG
GTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGGTCCCAGTGCCTCT
50 ATTGACAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCACATTGAATTCTCTG
ATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGCTGAGGAGAGAT
GTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTGTAG (SEQ ID NO:
164)

AOLFR89 sequences:

55 MLDPSISSHTLYLHSLFPQGLRKGTMWQKNQTSADFILEGLFDDSLTHLFLSLTMVVFLIAVS
GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTIILKMATNYLSGKKSISFVGCATQHFLYL

CLGGAECFLLAVMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWL GASVNSLIHMAILMHF
PFCGPRKVYHFYCEFPVVKLVCGDITVYETTVYISSILLLLPIFLISTSYVFIQSVIQMRSSGSK
RNAFATCGSHLTVVSLWFGACIFS YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVA
KALRRVLRRDVITQCIQRLQLWLPRV (SEQ ID NO: 165)

5

ATGCTGGACCCAGTATTTCCAGTCACACTCTTTATCTCCACTCTCTGTTTCCTCAGGGATT
GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGG
GCTCTTCGATGACTCCCTTACCCACCTTTTCTCTCTGACCATGGTGGTCTTCCTTAT
TGCGGTGAGTGGCAACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACA
CCAATGTATTTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT
CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA
ACCCAGCACTTCCTCTATTTGTGTCTAGGTGGTGTGAATGTTTCTCTTAGCTGTCTATGTC
CTATGACCGCTATGTTGCCATCTGTCTCATCCACTGCGCTATGCTGTGCTCATGAACAAGAAG
GTGGGACTGATGATGGCTGTCTGTCTGTTGGGGGCATCCGTGAACTCCCTAATTACACA
TGCGCATCTTGATGCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGA
GTTCACAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC
ATCAGCAGCATTCTCCTCCTCCTCCCATCTTCTGATTCTTACATCCTATCTTCTCATCCTT
CAAAGTGTCTATCAGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCT
CCCACCTCACGGTGGTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCTACATGAGACCCAGG
TCCCAGTGCATCTATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCA
CATTGAATTCTCTGATTATATACTCTCCGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT
GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTG
TAG (SEQ ID NO: 166)

25

AOLFR90 sequences:

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQPNVQEI VVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
TPKMI VDSLVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
CGILMGVAWTGGLHSMIQLFTFQLPFCGPNVINHFMC DLYLLELACTDTHIFGLMVVINS
G FICINFSLLLVS YAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYIILNPLL NPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 167)

30

ATGTTCTCAATGACAACAGAAAGCACTCAATAATTTTGCACTTGGATGTACCAACTTGTTAA
TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCTTTGTCCTAATTGCAGACTATA
CATGATCCCTGTTGGAGCTTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCTCTGGGACTTTACAGAATCCAAATGTTTCAGGAAATAGTATTTGTTG
TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATCTC
AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGTCTTCTCTGGA
TGCGTGCTTCTCATCTGTCTACCCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTGTCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
GGCCTCTTGCAATCCATGATACAAATTCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
ACATCTTTGGCCTCATGGTGGTGCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTCTCTTGTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA
TATTTGTATATACACGACCTCCATCTGCTTTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 168)

50

AOLFR91 sequences:

MGNWSTVTEITLIAFPALLEIRISLFVVLVVTYTLTATGNITHISLIWIDHRLQTPMYFFLSNLSFL
DILYTTVITPKLLACLLGEEKTISFAGCMIQTYFYFFLGTVFILLAVMSFDRYMAICDPLHYTVI
MNSRACLLLVLCWVGAFLSVLFPTIVVTRLPYCRKEINHFFCDIAPLLQVACINTHLIEKINFL

55

SALVILSSLAFTTGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSL
YDKVA AVLITVVTPLLPFIYSLRNEKVQEVLR ETVNRIMTLIQRKT (SEQ ID NO: 169)

5 ATGGGAAACTGGAGCACTGTGACTGAAATCACCCCTAATTGCCTTCCCAGCTCTCCTGGAGA
TTCGAATATCTCTCTCGTGGTTCTTGTGGTAACTTACACATTAACAGCAACAGGAAACAT
CACCATCATCTCCCTGATATGGATTGATCATCGCCTGCAAACCTCCAATGTACTTCTCCTCA
GTAATTTGTCCTTTCTGGATATCTTATACACCACTGTCATTACCCCAAAGTTGTTGGCCTGC
CTCCTAGGAGAAGAGAAAACCATATCTTTTGCTGGTTCATGATCCAAACATATTTCTACT
TCTTCTGGGGACGGTGGAGTTTATCCTCTTGGCGGTGATGTCCTTTGACCGCTACATGGC
10 TATCTGCGACCCACTGCACTACACGGTCATCATGAACAGCAGGGCCTGCCTTCTGCTGGTT
CTGGGATGCTGGGTGGGAGCCTTCTGTCTGTGTTGTTTCCAACCATGTAAGTACAAAGGC
TACCTTACTGTAGGAAAGAAATTAATCATTCTTCTGTGACATTGCCCTCTTCTTCAGGTG
GCCTGTATAAAATACTCACCTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTTGTCATCCT
GAGCTCCCTGGCATTCACTACTGGGTCTACGTGTACATAATTTCTACCATCCTGCGTATCC
15 CCTCCACCCAGGGCCGTCAGAAAGCTTTTCTACCTGTGCTTCTCACATCACTGTTGTCTCC
ATTGCCCACGGGAGCAACATCTTTGTGATGTGAGACCCAATCAGAACTCCTCACTGGATT
ATGACAAGGTGGCCGCTGTCCTCATCACAGTGGTGACCCCTCTCCTGAACCCCTTTATCTA
CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTGAGAGAGACAGTGAACAGAATCATGAC
CTTGATACAAAGGAAACTTGA (SEQ ID NO: 170)

20

AOLFR92 sequences:

MRNGTVITEFILLGFPVIQGLQTPLFIAIFLTYILTLAGNGLIATVWAEPRQLQIPMYFFLCNLSFLE
IWYTTTVPKLLGTFVVARVICMSCCLLQAFHHFVGTTEFLILTIMSFDRYLTCNPLHPTIM
TSKLCLQLALSSWVVGFTIVFCQTMILLIQLPFCGNNVISHFYCDVGPSLKAACIDTSILELLGVIA
25 TILVIPGSLLFNMISYIYILSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK
INKVSVLNTILTPLLNPFIYTIRNKEVKGALRKAMTCPKTGHAK (SEQ ID NO: 171)

ATGAGAAATGGCACAGTAATCACAGAATTCATCCTGCTAGGCTTTCCTGTTATCCAAGGCC
TACAAACACCTCTCTTTATTGCAATCTTTCTCACCTACATATTAACCTTGCAGGCAATGGG
30 CTTATTATTGCCACTGTGTGGGCTGAGCCAGGCTACAAATCCAATGTACTTCTTCCTTTG
TAAACTTGTCTTTCTTAGAAATCTGGTACACACCAAGTCATCCCCAAACTGCTAGGAACC
TTTGTAGTGGCAAGAACAGTAATCTGCATGTCCTGCTGCCTGCTGCAGGCCTTCTTCCACT
TCTTCGTGGGCACCACCGAGTTCTTGATCCTCACTATCATGTCTTTTGACCGCTACCTCACC
ATCTGCAATCCCCTTACCACCCACCATCATGACCAGCAAACTCTGCCTGCAGCTGGCCC
35 TGAGCTCCTGGGTGGTGGGCTTACCATTGTCTTTTGTGACGATGCTGCTCATCCAGTT
GCCATTCTGTGGCAATAATGTTATCAGTCATTTCTACTGTGATGTTGGGCCAGTTTGAAA
GCCGCCTGCATAGACACCAGCATTTTGGAACTCCTGGGCGTCATAGCAACCATCCTTGTGA
TCCCAGGGTCACTTCTCTTTAATATGATTCTTATATCTACATTCTGTCCGCAATCCTACGA
ATTCTTCAGCCACTGGCCACAAAAGACTTTCTCTACCTGTGCCTCGCACCTGACAGTTGT
40 CTCCCTGCTCTACGGGGCTGTTCTGTTCATGTACCTAAGACCCACAGCACACTCCTCCTTTA
AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCCTCACCCCTTCTGAATCCCTTTATT
TATACTATTAGAAACAAGGAGGTGAAGGGAGCCTTAAGAAAGGCAATGACTTGCCCCAAG
ACTGGTCATGCAAGTAA (SEQ ID NO: 172)

45 **AOLFR93 sequences:**

MLMNYSSATEFYLLGFPGSEELHHILFAIFFFFYLVTLMGNTVIIMIVCVDKRLQSPMYFFLGHL
SALEILVTTHVPVMLWGLLLPGMQTIYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN
PLRYNIIMNRHTCNFVVLVSWVFGFLFQIWPVYVMFQLTYCKSNVNNFFCDRGQLKLSCN
NTLFTEFILFLMAVFVLFGLIPTIVSNAYIISTILKIPSSSGRRKSFTCASHFTCVVIGYGSCLFLY
50 VKPKQQTQAADYNWVVSMLMSVVTPLNPFIETLRNDKVIEALRDGVKRCCQLFRN (SEQ ID
NO: 173)

ATGTTGATGAATTACTCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA
55 ACTACATCATATCCTTTTTGCTATATTCTTCTTTTCTACTTGGTGACATTAATGGGAAACA
CAGTCATCATCATGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCCTC
GGCCACCTCTCTGCCCTGGAGATCCTGGTCACAACCATAATCGTCCCCGTGATGCTTTGGG

GATTGCTGCTCCCTGGGATGCAGACAATATATTTGTCTGCCTGTGTTGTCCAGCTCTTCTTG
TACCTTGCTGTGGGGACAACAGAGTTCGCATTACTTGGAGCAATGGCTGTGGACCGTTATG
TGGCTGTCTGTAACCCCTCTGAGGTACAACATCATTATGAACAGACACACCTGCAACTTTGT
GGTCTTGTGTGTCATGGGTGTTTGGGTTTCTTTTCAAATCTGGCCGGTCTATGTCATGTTTC
5 AGCTTACTTACTGCAAATCAAATGTGGTGAACAATTTTTTTGTGACCGAGGGGCAATTGCT
CAAATATCCTGCAATAATACTCTTTTACGGAGTTTATCCTCTTCTTAATGGCTGTTTTG
TTCTCTTTGGTTCTTTGATCCCTACAATTGTCTCCAACGCCTACATCATCTCCACCATTCTC
AAGATCCCGTCATCCTCTGGCCGGAGGAAATCCTTCTCCACTTGTGCCTCCCACTTCACCTG
TGTGTGATTGGCTACGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACGCAGGCA
10 GCTGATTACAATTGGGTAGTTTCCCTGATGGTTTCAGTAGTAACTCCTTTCCTCAATCCTTT
CATCTTCACCCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC
TGCAACTATTCAGGAATTAG (SEQ ID NO: 174)

AOLFR94 sequences:

15 METWVNQSYTDGFFLLGIFSHSTADLVLSVVMVFTVALCGNVLLIFLIYMDPHLHTPMYFF
LSQLSLMDLMLVCTNPVKMAANFLSGRKSISFVCGIQLFVCLVSGEGLLLGLMAYDRYVA
ISHPLHYPLMNQRVCLQITGSSWAFGIIDGLIQMVVVMNFPYCGLRKVNHFCEMLSLLKLAC
VDTSLFEKVIFACCVFMLLPFSIIVASYAHILGTVLQMHSQAQWKKALATCSSHLTAVTLFYG
AAMFIYLRPRHYRAPSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGLDRCRIGSQH
20 (SEQ ID NO: 175)

ATGGAGACGTGGGTGAACCAGTCTACACAGATGGCTTCTTCTCTTAGGCATCTTCTCCC
ACAGTACTGCTGACCTTGTCTCTTCTCCGTGGTTATGGCGGTCTTCACAGTGGCCCTCTGT
GGGAATGTCTCCTCATCTTCTCATCTACATGGACCCTCACCTTCACACCCCCATGTACTT
25 CTCTCCTCAGCCAGCTCTCCCTCATGGACCTCATGTGCTGTACCAATGTGCCAAAGATG
GCAGCCAACTTCTGTCTGGCAGGAAGTCCATCTCCTTTGTGGGTGTGGCATACAAATG
GCCTCTTTGTCTGTCTTGTGGGATCTGAGGGGCTCTTGCTGGGACTCATGGCTTATGACCG
CTATGTGGCCATTAGCCACCCACTTCACTATCCCATCCTCATGAATCAGAGGGTCTGTCTCC
AGATTACTGGGAGCTCCTGGGCCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT
30 AATGAATTTCCCCTACTGTGGCTTGAGGAAGGTGAACCATTTCTTCTGTGAGATGCTATCC
TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAGAAGGTGATATTGCTTGCTGTG
TCTTCATGCTTCTTCTCCCATCTCCATCATCGTGGCCTCCTATGCTCACATTCTAGGGACT
GTGCTGCAAATGCACTCTGCTCAGGCCTGGAAAAAGGCCCTGGCCACCTGCTCCTCCCACC
TGACAGCTGTCAACCCTCTTCTATGGGGCAGCCATGTTTCATCTACCTGAGGCCTAGGCACTA
35 CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGTCTTACTCCCATGCTC
AACCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGCACTGAGGAAGGGGCTG
GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

AOLFR95 sequences:

40 MLGSKPRVHLYILPCASQQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILLFLLFLFVYAMILL
GNVGMMTIIMTDPRLNTPMYFFLGNLSFIDLFIYSSVIEPKAMINFWSENKSISFAGCVAQLFLFA
LLIVTEGFLLAAMAYDRFIAICNPLLYSVQMSTRCTQLVAGSYFCGCISSVIQTSMTFTLSFCAS
RAVDHFYCDSPRLQRLSCSDLFIHRMISFSLSCIILPTIIVSYMYIVSTVLKIHSTEGHKKAFST
CSSHLGVVSVLYGAVFFMYLTPDRFPELSKVASLCYSLVTPMLNPLIYSLRNKDVQEALKKFLE
45 KKNIL (SEQ ID NO: 177)

ATGCTAGGATCCAAACCAAGAGTTCATTTGTATATTTTGCCCTGTGCCTCTCAACAGGTTTC
TACCATGGGTGACAGGGGAACAAGCAATCACTCAGAAATGACTGACTTCATTCTTGCAGG
CTTCAGGGTACGCCCAGAGCTCCACATTCTCCTCTTCTGCTATTTTTGTTTGTATGCCA
50 TGATCCTTCTAGGGAATGTTGGGATGATGACCATTATTATGACTGATCCTCGGCTGAACAC
ACCAATGTATTTTTTCTAGGCAATCTCCTTCATTGATCTTTTCTATTCTGTTATTGA
ACCCAAGGCTATGATCAACTTCTGGTCTGAAAACAAGTCTATCTCCTTTGCAGGCTGTGTG
GCCAGCTCTTTCTCTTTGCCCTCCTCATTGTGACTGAGGGATTTCTCCTGGCGCCATGGC
TTATGACCGCTTTATTGCCATCTGCAACCCTCTGCTCTACTCTGTTCAAATGTCCACACGTC
55 TGTGTACTCAGTTGGTGGCTGGTTCTATTTTTGTGGCTGCATTAGCTCAGTTATTCAGACT
AGCATGACATTTACTTTATCTTTTTGCGCTTCTCGGGCTGTTGACCACTTTACTGTGATTC

TCGCCCACCTTCAGAGACTGTCTTGTCTGATCTCTTTATCCATAGAATGATATCTTTTTCT
TATCATGTATTATTATCTTGCCTACTATCATAGTCATTATAGTATCTTACATGTATATTGTG
TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT
CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGCTGTCTTTTTATGTATCTCACTCCTGAC
5 AGATTTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTTGA
ATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAATTTCTAGA
GAAGAAAAATATTATTCTTTGA (SEQ ID NO: 178)

AOLFR96 sequences:

10 MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAIYTVTLLGNFLIVTVTSVDLALQTPMYFFLQ
LSLLEVCFVLVMVPKMLVDLVSPRKIISFVCGTQMYFFFFGSSECFLLSMMA YDRFVAICNP
LHYSVIMNRSCLWMAIGSWMSGVPVSMQLTAWMMALPFCGPNAVDFHFCGPPVLKLVTV
DTTMYEMQALASTLLFIMFPFCLILVSYTRIIITILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL
TYLRPKSNQSPESKKLVLSYTVITPMLNPIIYGLRNNNEVKGAVKRTITQKVLQKLDVF (SEQ
15 ID NO: 179)

ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATTCTTCTTGGTTTTACAAACAACC
CCGAGATGCAAGTTTCCCTCTTTATTTTTTCTGGCCATTTATACAGTCACTTTGTTGGGC
AATTTCTTATTGTACAGTTACCACTGTGGATCTCGCACTTCAAACACCCATGTACTTCTT
20 TCTTCAAATCTGTCACTTCTTGAAGTATGTTTACCTTGGTTATGGTGCCAAAAATGCTTG
TAGATCTAGTGTCCCAAGGAAAATTATCTCTTTTGTGGGCTGTGGTACCCAGATGTACTT
CTTCTTCTTCTTGGCAGTTCTGAATGTTTCTTCTCTCCATGATGGCTTATGATCGCTTTGT
GGCATCTGTAACCTCTCCATTATTCAGTCATAATGAACAGGTCCCTATGCTTGTGGATG
GCCATAGGCTCTTGGATGTCCGGTGTCTCTGTGCTATGCTACAGACAGCTTGGATGATGG
25 CCTTCCTTTCTGTGGACCAAATGCCGTGGACCACTTTTTCTGTGATGGTCCCCCAGTGTTA
AACTAGTCACAGTGGATACAAACCATGTATGAAATGAAGCACTGCCTCCACACTCCTGT
TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTTACACCCGCATTATCATAACAATTCTG
AGGATGTCTCTGCCACTGGCCGCCAGAAGGCATTTTCTACTTGTTCCTCACACCTCATTGT
GGTGCCCTCTTCTACGGAACAGCCAGTCTGACCTACCTGCGGCCCAAATCAAACCACTCC
30 CCTGAGAGCAAGAAGCTAGTGTCTTCTACACTGTCATCACACCTATGCTAAACCCCA
TCATCTACGGCCTGAGGAACAATGAAGTGAAGGGGCTGTCAAGAGGACAATCACTCAA
AAGTCTTACAGAAGTTAGATGTGTTTTGA (SEQ ID NO: 180)

AOLFR97 sequences:

35 MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSMFVVPFSIAEHWRRMKGANLSQGMFEL
LGLTTDPQLQRLLFVFLGMYTATLLGNLVMFLLIHVSATLHTPMYSLKSLSLDFCYSSTVV
PQTLVNFLAKRKVISYFGCMTQMFFYAGFATSECYLIAAMAYDRYAAICNPLLYSTIMSPEVC
ASLIVGSYSAGFLNSLIHTGCIFSLKFCGAHVVTTHFFCDGPPILSLSCVDTSLEILLFIFAGFNLLS
CTLTILISYFLILNTILKMSSAQGRFKAFTSCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRTVA
40 VIYTVVIPVLNPLMYSLRNKDVKKALIKVWGRKTME (SEQ ID NO: 181)

ATGACAGAGTTTCATCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAGGCTGT
CCTTAGGCAGAAATTAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTTATGGTGGTGCC
TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAAACCTGAGCCAAGGGAT
45 GGAGTTTGAGCTCTTGGGCCTCAACCTGACCCCCAGCTCCAGAGGCTGCTCTTCGTGGTG
TTCCTGGGCATGTACACAGCCACTCTGCTGGGGAACCTGGTCATGTTCTCTCTGATCCATG
TGAGTGCCACCCTGCACACACCCATGTACTCCCTCCTGAAGAGCCTCTCCTTCTTGGATTTC
TGCTACTCCTCCACGGTTGTGCCCCAGACCTGGTGAACCTTCTTGGCCAAGAGGAAAGTGA
TCTCTTATTTTGGCTGCATGACTCAGATGTTCTTCTATGCGGGTTTTGCCACCACTGAGTGC
50 TATCTCATCGCTGCCATGGCCTATGACCGCTATGCCGCTATTTGTAACCCCTGCTCTACTC
AACCATCATGTCTCCTGAGGTCTGTGCTCGCTGATTGTGGGCTCCTACAGTGCAGGATTC
CTCAATTCTCTTATCCACACTGGCTGTATCTTAGTCTGAAATTCTGCGGTGCTCATGTGCT
CACTCACTTCTTCTGTGATGGGCCACCCATCCTGCTCTTGTCTTGTGTAGACACCTCACTGT
GTGAGATCCTGCTCTTCAATTTTGTGCTGGTTTCAACCTTTTGAAGCTGCACCCCTCACTCTTG
55 ATCTCCTACTTCTTAATTTCTCAACACCATCCTGAAAATGAGCTCGGCCAGGGCAGGTTA
AGGCATTTTCCACCTGTGCATCCACCTCACTGCCATCTGCTCTTCTTTGGCACAACTT

TTTATGTACCTGCGCCCCAGGTCCAGCTACTCCTTGACCCAGGACCGCACAGTTGCTGTCA
TCTACACAGTGGTGATCCCAGTGCTGAACCCCTCATGTACTCTTTGAGAAACAAGGATGT
GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)

5 **AOLFR98 sequences:**

MRGFNKTTVVTFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGFLEI
LSFSESCYTFVIIPQLLVHLLSDTKTISFMACATQLFFFLGFACTNCLLIAVMGYDRYVAICHPLR
YTLIINKRLGLELISLSGATGFFIALVATNLICDMRFCGPNRVNHYFCDMAPVIKLACTDTHVKE
10 LALFSLSILVIMVPFLILISYGFIVNTILKIPSAEGKKAFVTCASHLTVVVFVHYGCASIIYLRPKSK
SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)

ATGCGAGGTTTCAACAAAACCACTGTGGTTACACAGTTCATCCTGGTGGGTTTCTCCAGCC
TGGGGGAGCTCCAGCTGCTGCTTTTTGTGCTCTTTCTTCTCCTATACTTGACAATCCTGGTG
GCCAAATGTGACCATCATGGCCGTTATTCGCTTCAGCTGGACTCTCCACACTCCCATGTATG
15 GCTTTCTATTCTCCTTTTCTGAGTCTGCTACACTTTTGTGCTATCCTCAGCTGCTG
TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTTCATGGCCTGTGCCACCCAGCTGTT
CTTTTCTCTGGCTTTGCTTGACCAACTGCCTCCTCATTGCTGTGATGGGATATGATCGCT
ATGTAGCAATTTGTGACCCCTCTGAGGTACACACTCATATAACAAAAGGCTGGGGTTGGA
GTTGATTTCTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGGCCACCAACCTCATTT
20 GTGACATGCGTTTTTGTGGCCCCAACAGGGTTAACCCTATTCTGTGACATGGCACCTGT
TATCAAGTTAGCCTGCACTGACACCCATGTGAAAGAGCTGGCTTTATTTAGCCTCAGCATC
CTGGTAATTATGGTGCTTTTCTGTAAATTCTCATATCCTATGGCTTCATAGTTAACACCAT
CCTGAAGATCCCCCTCAGCTGAGGGCAAGAAGGCCTTTGTACCTGTGCCTCACATCTCACT
GTGGTCTTTGTCCACTATGGCTGTGCCTCTATCATCTATCTGCGGCCCAAGTCCAAGTCTGC
25 CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTTACTCCCTTACTTAATCCT
CTTGTCTACAGTCTGAGGAACAAAGAGGTAAAACTGCATTGAAAAGAGTTCTTGGAATG
CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

AOLFR99 sequences:

30 MERVNETVVREVIFLGFSSLARLQQLLFVIFLLLYLFTLTGTNAIISTIVLDRALHIPMYFFLAILSC
SEICYTFIIVPKMLVDLLSQKKTISFLGCAIQMFSFLFLGCSHSFLLAVMGYDRYIAICNPLRYSV
LMGHGVCMLGVAAACACGFTVAQIITSLVFHLPFYSSNQLHHFFCDIAPVLKLASHHNHFSQIV
IFMLCTLVLAIPLLLILVSYVHILSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASFIYLRPQSNY
SSSQDALISVSYTIITPLFNPMIYSLRNKEFKSALCKIVRRTISLL (SEQ ID NO: 185)

35 ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTTCATCTTCCTCGGCTTCTCATCCCTGG
CCAGGTGCGAGCAGCTGCTCTTTGTTATCTTCTGCTCCTCTACCTGTTCACTCTGGGCACC
AATGCAATCATCATTTCCACCATGTCCTGGACAGGGCCCTTCATATCCCCATGACTTCTT
CCTTGCCATCCTCTCTTGCTCTGAGATTGTGACACCTTCATCATTGTACCCAGATGCTGG
40 TTGACCTGCTGTCCCAGAAGAAGACCATTTCTTTCTGGGCTGTGCCATCCAAATGTTTTCC
TTCCTCTTCCTTGGCTGCTCTCACTCCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT
AGCCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTGTATGGGACTA
GTGGCTGCTGCCTGTGCCTGTGGCTTCACTGTTGCACAGATCATCACATCCTTGGTATTTC
CCTGCCTTTTTATTCTCCAATCACTACATCACTTCTTCTGTGACATTGCTCCTGTCTCA
45 AGCTGGCATCTCACCATAACCACTTTAGTCAGATTGTCATCTTCATGCTCTGTACATTGGTC
CTGGCTATCCCCCTATTGTTGATCTTGGTGTCTATGTTTACATCCTCTCTGCCATACTTCA
GTTTCCTTCCACACTGGGTAGGTGCAAAGCTTTTTCTACCTGTGTATCTCACCTCATTATTG
TCACTGTCCACTATGGCTGTGCCTCCTTTATCTACTTAAGGCCTCAGTCCAACCTACTCCTCA
AGCCAGGATGCTCTAATATCAGTATCCTACACTATTATAACTCCATTGTTCAACCCAATGA
50 TTTATAGCTTGAGAAATAAAGAGTTCAAATCAGCTCTTTGTAAATTGTGAGAAGAACAAT
TTCCCTGTTGTAA (SEQ ID NO: 186)

AOLFR101 sequences:

MDTGNWSQVAEFIILGFPHLQGVQIYLFLLLLLIYLMTVLGNLLIFLVVCLDSRLHTPMYHFVSI
55 LSFSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL
HYPTLMTPTLCAEIAIGCWLGLAGPVVEISLISRLPFCGPNRIQHVFCDFFPVLSLACTDTSINV

CAGTGCTGCTGGAGCATGGGGCAGCTTTATCTTACACACGCTGTGCTGCTCAGTTCTTTCT
GTTACCTTCTTTGGTTCCATCGACTGCTACCTCTTGGCCCTCATGGCCTATGACCGCTACT
TGGCTGTGTGCCAGCCCCTGCTTTATGTACCATCCTGACACAGCAGGCCCGCTTGAGTCT
TGTGGCTGGGGCTTACGTTGCTGGTCTCATCAGTGCCTTGGTGCGGACAGTCTCAGCCTTC
5 ACTCTCTCCTTCTGTGGAACCAAGTGAAGATTGACTTTATTTTCTGTGACCTCCCTCCTCTGTT
AAAGTTGACCTGTGGGGAGAGCTACACTCAAGAAGTGTGATTATTATGTTTGCCATTTTT
GTCATCCCCTGCTTCCATGGTGGTGATCTTGGTGTCTTACCTGTTTATCATCGTGGCCATCAT
GGGGATCCCCTGCTGGAAGCCAGGCCAAGACCTTCTCCACCTGCACCTCCCACCTCACTGCT
GTGTCACTCTTCTTTGGTACCCTCATCTTCATGTACTTGAGAGGTAACCTCAGATCAGTCTTC
10 GGAGAAGAATCGGGTAGTGTCTGTGCTTTACACAGAGGTATCCCCATGTTGAATCCCCCTC
ATCTACAGCCTGAGGAACAAGGAAGTGAAGGAGGCCCTGAGAAAAATTCTCAATAGAGCC
AAGTTGTCCTAA (SEQ ID NO: 192)

AOLFR105 sequences:

15 MQGLNHTSVSEFILVGFSAPHLQLMLFLLFLLMYLFTLLGNLLIMATVWSERSLHMPMYLFLC
ALSITEILYTVAIIPRLADLLSTQRSIAFLACASQMFFSFSFGFTHSFLLTVMGYDRYVAICHPL
RYNVLMRLRGCTCRVGCWSWAGGLVMGMVVTSAIFHLAFCGHKEIHFFCHVPPLKLACGDD
VLVVAKGVLVCITALLGCFLILLISYAFIVAAILKIPSAEGRNKAFSTCASHLTVVVVHYGFAS
VIYLPKPGQSPGDTLMGITYTVLTPFLSPIHSLRNKELKVAMKKTCTFKLPQNC (SEQ ID
20 NO: 193)

ATGCAGGGGCTAAACCACACCTCCGTGTCTGAATTCATCCTCGTTGGCTTCTCTGCCTTCCC
CCACCTCCAGCTGATGCTCTTCTGCTGTTCTGCTGATGTACCTGTTACGCTGCTGGGCA
ACCTGCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCATGTACCTCTT
25 CCTGTGTGCCCTCTCCATACCGAGATCCTCTACACCGTGGCCATCATCCCGCGCATGCTG
GCCGACCTGCTGTGCCACCCAGCGCTCCATCGCCTTCCCTGGCCTGTGCCAGTCAGATGTTCTT
CTCCTTCAGCTTCGGCTTACCCACTCCTTCTGCTCACTGTCTGCGCTACGACCGCTACG
TGGCCATCTGCCACCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG
GGTGGGCTGCTCCTGGGCTGGTGGCTTGGTCACTGGGGATGGTGGTGACCTCGGCCATTTTC
30 CACCTCGCCTTCTGTGGACACAAGGAGATCCACCATTTCTTCTGCCACGTGCCACCTCTGTT
GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGTAT
CACGGCCCTGCTGGGCTGTTTTCTCCTCATCCTCCTCTCCTATGCCTTCATCGTGGCCGCCA
TCTTGAAGATCCCTTCTGCTGAAGGTGCGGAACAAGGCCTTCTCCACCTGTGCCTCTCACCT
CACTGTGGTGGTGCCTGCACTATGGCTTTGCCTCCGTCAATTTACCTGAAGCCCAAAGGTCCC
35 CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACTACACGGTCTCACACCTTCTCTCA
GCCCCATCATCTTACGCTCAGGAACAAGGAGCTGAAGGTGCGCATGAAGAAGACTTGCTT
CACCAAACCTCTTCCACAGAACTGCTGA (SEQ ID NO: 194)

AOLFR106 sequences:

40 METANYTKVTEFVLTGLSQTPEVQLVLFVIFLSFYLFILPGNILICTISLDPHLTSPMYFLLANLA
FLDIWYSSITAPEMLIDFFVERKIIISFDGCIQFLFLHFAGASEMFLLTVMMAFDLYTAICRPLHYA
TIMNQRLCCILVALSWRGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
ICSSGLISVVCLIALMSYAFLALFKKLSGSGENTNRAMSTCYSHITIVVLMFGPSIYIYARFDF
SFSLDKVVSFVNTLIFPLRNPIIYTLRNKEVKAAMRKLVTKYILCKEK (SEQ ID NO: 195)

45 ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
CAGAGGTCCAACCTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
AATATCCTTATCATTGACCATCAGTCTAGACCCTCATCTGACCTCTCCTATGTATTTCCT
GTTGGCTAATCTGGCCTTCTTGATATTTGGTACTCTTCCATTACAGCCCTGAAATGCTCA
50 TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTTGATGGATGCATTGCACAGCTCTTCTT
CTTACACTTTGCTGGGGCTTCGGAGATGTTCTTGCTCACAGTGATGGCCTTTGACCTCTACA
CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGTCTCTGCTGTATCCTG
GTGGCTCTCTCCTGGAGGGGGGGCTTCATTCTATCATACAGGTGGCTCTCATTGTTTC
GACTTCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTGTG
55 CCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCTG
ATCTCTGTGGTGTGTTTGATTGCTCTGTTAATGTCTATGCCTTCTTCTGGCCTTGTTCAA

AOLFR109 sequences:

MLRNGSIVTEFILVGFQSSSTSTRALLFALFLALYSLTMAMNGLIIFITSWTDPKLNSPMYFFLG
HLSLLDVCFITTTIPQMLIHLVVRDHIVSFVCCMTQMYFVFCVGAECILLAFMAYDRYVAICY
5 PLNYVPIISQKVCVRLVGTAWFFGLINGIFLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPQFSL
WAIFADAIVVILSPMVLTVTSYVHILATILSKASSSGRGKTFSTCASHLTVVIFLYTSAMFSYMN
PHSTHGPDKDKPFSLLYTHTPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPQSV (SEQ ID NO:
201)

10 ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTTCAGCAGAGCTCCA
CTTCCACACGAGCATTGCTCTTTGCCCTCTTCTTGGCCCTCTACAGCCTCACCATGGCCATG
AATGGCCTCATCATCTTTATCACCTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTACT
TCTTCCCTCGGCCATCTGTCTCTCCTGGATGTCTGCTTCATCACCCTACCATCCCACAGATG
TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT
15 ACTTTGTCTTCTGTGTTGGTGTGGCCGAGTGCATCCTCTTGGCTTTTCATGGCCTATGACCGT
TATGTTGCTATCTGCTACCCACTTAAGTATGTCCCGATCATAAGCCAGAAGGTCTGTGTCA
GGCTTGTGGGAAGTGCCTGGTTCTTTGGGCTGATCAATGGCATCTTTCTCGAGTATATTTTC
ATTCCGAGAGCCCTTCCGCAGAGACAACACATAGAAAGCTTCTTCTGTGAGGCCCCCATA
GTGATTGGCCTCTCTTGTGGGGACCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA
20 TCGTGGTAATTCTCAGCCCCATGGTGCTCACTGTCACCTCCTATGTGCACATCCTGGCCACC
ATCCTCAGCAAAGCCTCCTCCTCAGGTGCGGGGAAGACTTTCTCTACTTGTGCCTCTCACC
TGACTGTGGTCATCTTTCTCTACACTTCAGCTATGTTCTCTTACATGAACCCCCACAGCACA
CATGGGCCTGACAAAGACAAACCTTTCTCCCTCCTGTACACCATCATTACCCCCATGTGCA
ACCCCATCATTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTG
25 GAAGAACCAGGCTGGCCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

AOLFR110 sequences:

MKIANNVTVTEFILLGLTQSQDIQLLVFVLILIFYLILPGNFIIFTIRSDPGLTAPLYLFLGNLAFL
DASYSFIVAPRMLVDFLSEKKVISYRGCIQLFFLHFLGGEGLLLVMAFDRYIAICRPLHCST
30 VMNPRACYAMMLALWLGGFVHSIIQVVLRLPFCGPNQLDNFFCDVRQVIKLACTDMFVVEL
LMVFNISGLMTLLCFLGLLASYAVILCHVRRASEGKNKAMSTCTTRVIIIIMFGPAIFIYMCPP
RALPADKMVSLFHTVIFPLMNPMIYTLRNQEVKTSMKRLLSRHVVCQVDFIIRN (SEQ ID NO:
203)

35 ATGAAGATAGCAAACAACACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC
AAGATATTCAGCTCTTGGTCTTTGTGCTGATCTTAATTTTCTACCTTATCATCCTCCCTGGA
AATTTTCTCATTATTTTACCATAAGGTCAGACCCTGGGCTCACAGCCCCCTCTATTTATT
TCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTCATTGTGGCTCCCAGGATGTTGG
TGGACTTCCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTTT
40 CTTGCACTTCCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTAC
ATCGCCATCTGCCGGCCTCTGCACTGTTCAACTGTCATGAACCCTAGAGCCTGCTATGCAA
TGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCCCTCATCCTC
CGCTTGCCTTTTTGTGGCCCAAACCAGCTGGACAACTTCTTCTGTGATGTCCGACAGGTCA
TCAAGCTGGCTTGCACCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT
45 GATGACACTCCTGTGCTTTCTGGGGCTTCTGGCTTCTATGCAGTCATCCTCTGCCATGTTCT
GTAGGGCAGCTTCTGAAGGGAAGAACAAGGCCATGTCCACGTGCACCACTCGTGTCTATTA
TTATACTTCTTATGTTTGGACCTGCTATCTTCATCTACATGTGCCCTTTCAGGGCCTTACCA
GCTGACAAGATGGTTTCTCTCTTTCACACAGTGATCTTCCATTGATGAATCCTATGATTTA
TACCTTTCGCAACCAGGAAGTGAAAACCTCCATGAAGAGGTTATTGAGTCGACATGTAGTC
50 TGTCAAGTGGATTTTATAATAAGAACTGA (SEQ ID NO: 204)

AOLFR111 sequences:

MCYIYLIFKEWTLIFYFSLLLFLQITPAIMANLTIVTEFILMGFSTNKNMCILHSILFLLIYLCALM
GNVLIIMITLTDHHLHTPVYFFLKNLSFLDLCLISVTAPKSIANSIHNNSISFLGCVSQVFLLS
55 ASAELLLLTVMSFDRYTAICHPLHYDVMIDRSTCVQRATVSWLYGGLIAVMHTAGTFSLSYCG
SNMVHQFFCDIPQLLAISCENLIREIALILINVLDFFCFIVIIITYVHVSTVKKIPSTEGQSKAY

SICLPHLLVVLFLSTGFIAYLKPASESPSILDAVISVFYTMLPPTFNPIIYSLRNKAIKVALGMLIKG
KLTKK (SEQ ID NO: 205)

5 ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT
TTTCCTGCAGATTACTCCTGCAATAATGGCAAATCTCACAATCGTGACTGAATTTATCCTTA
TGGGGTTTTCTACCAATAAAAAATATGTGCATTTTGCATTTCGATTCTCTTCTTGTTGATTAT
TTGTGTGCCCTGATGGGGAATGTCCTCATTATCATGATCACAACCTTTGGACCATCATCTCC
ACACCCCCGTGTATTTCTTCTTGAAGAATCTATCTTTCTTGGATCTCTGCCTTATTTTCAGTC
ACGGCTCCCAAATCTATCGCCAATTCTTTGATACACAACAACCTCCATTTTCATTCCTTGGCTG
10 TGTTTCCCAGGTCTTTTGTGTCTTTCTTTCAGCATCTGCAGAGCTGCTCCTCCTCACGGTGA
TGTCCTTTGACCGCTATACTGCTATATGTCCACCTCTGCACTATGATGTCATCATGGACAGG
AGCACCTGTGTCCAAAGAGCCACTGTGTCTTGGCTGTATGGGGGTCTGATTGCTGTGATGC
ACACAGCTGGCACCTTCTCCTTATCCTACTGTGGGTCCAACATGGTCCATCAGTTCTTCTGT
GACATTCCCCAGTTATTAGCTATTTCTTGCTCAGAAAAATTAATAAGAGAAATTGCACTCA
15 TCCTTATTAATGTAGTTTTGGATTTCTGCTGTTTTATTGTTCATCATCATTACCTATGTCCAC
GTCTTCTCTACAGTCAAGAAGATCCCTTCCACAGAAGGCCAGTCAAAAGCCTACTCTATTT
GCCTTCCACACTTGCTGGTTGTGTTATTTCTTCCACTGGATTCATTGCTTATCTGAAGCCA
GCTTCAGAGTCTCCTTCTATTTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCC
AACCTTTAATCCCATTATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG
20 TTGATAAAGGGAAAGCTCACCAAAAAGTAA (SEQ ID NO: 206)

AOLFR113 sequences:

MKFWHGFSSHLNPMFSSFLLYLSLPWINTTIQAWLNLCSLALPVWAMSGAGFLSCCYWHTCSP
SVVTCSSSQSSDWMQLCTHLCTTSLVFFPSWSCGIQLPLSLRCCLIFSRRKPFLLQDASFRPTSS
25 TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTTLCAKMAAACWTCGFLCPISEVILASQLPF
CAYNEIQHIFCDFPPLSLACKDTSANILVDFAINAFILITFFFIMISYARIIGAVLKIKTASGRKK
AFSTCASHLAVVLIFGSIIFMYVRLKKSYSYSLTLDRTLAIVSVLTPMVNPIIYSLRNKEIKAIKR
TIFQKGDKASLAHL (SEQ ID NO: 207)

30 ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTGGCTGGCTATCTCACTGA
GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
35 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
40 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
GCAGTCTCTACAGTCTGATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
AGCATTAAGCACATGTGGCTCCCATGTGGGGGTATGGCTTTGTACTATCTACCTGGGATG
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACACCAAGTCCTGC
45 TAGCTGACCTGTACGTGATCATCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
CAAACAACCTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
CTGGGTTCATGA (SEQ ID NO: 208)

AOLFR114 sequences:

50 MERINHTSSVSEFILLGLSSRPEDQKTLFVFLIVYLVTTIGNLLIILAIRFNPQLQTPMYFFLSFLS
LTDICFTTSVVPKMLMNFLEKKTISYAGCLTQMYFLYALGNSDSCLLAVMAFDYVAVCDPF
HYVTTMSHHHCVLLVAFSCSFPHLHSLHLLHTLLNRLTFCDNSVIHHFLCDLSPVLKLSCSSIFVN
EIVQMTEAPIVLVTRFLCIAFSYIRILTTVLKIPSTSGKRKAFSTCGFYLTVVTLFYGSIFCVYLQP
PSTYAVKDHVATIVYTVLSSMLNPFIIYSLRNKDLKQGLRKLMSKRS (SEQ ID NO: 209)

55

ATGGAAGAATCAACCACACCAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCCTCCC
GGCCTGAGGACCAAAAAGACACTCTTTGTTCTCTTCCCTCATCGTGACCTGGTCACCATAAC
AGGGAACCTGCTCATCATCTGGCCATTTCGTTCAACCCCCATCTTCAGACCCCTATGTATT
TCTTCTTGAGTTTTCTGTCTCTCACTGATATTTGCTTTACAACAAGCGTTGTCCCCAAGATG
5 CTGATGAACCTCCTGTCAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACACAGATGT
ATTTTCTCTATGCCTTGGGCAACAGTGACAGCTGCCTTCTGGCAGTCATGGCCTTTGACCG
CTATGTGGCCGTCTGTGACCCTTTCCACTATGTCAACCACCATGAGCCACCACCCTGTGTCC
TGCTGGTGGCCTTCTCCTGCTCATTTCCTCACCTCCACTCACTCCTGCACACACTTCTGCTG
AATCGTCTCACCTTCTGTGACTCCAATGTTATCCACCACTTTCTCTGTGACCTCAGCCCTGT
10 GCTGAAATTGTCCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACAGAAGCACCT
ATTGTTTTGGTGACTCGTTTTCTCTGCATTGCTTTCTCTTATATACGAATCCTCACTACAGT
TCTCAAGATTCCCTCTACTTCTGGGAAACGCAAAGCCTTCTCCACCTGTGGTTTTTACCTCA
CCGTGGTGACGCTCTTTTATGGAAGCATCTTCTGTGTCTATTTACAGCCCCCATCCACCTAC
GCTGTCAAGGACCACGTGGCAACAATTGTTTACACAGTTTTGTCATCCATGCTCAATCCTT
15 TTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCAAGA
GATCCTAG (SEQ ID NO: 210)

AOLFR115 sequences:

MEGFYLRRSHELQGMGKPGRVNQTTVSDFLLGLSEWPPEEQPLLFGIFLGMYLVTMVGNNLLII
20 LAISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLMFGGLD
NCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVLTNCPALMHTLLLRVAFCAQK
AIPHFYCDPSALLKLACSDTHVNELMIITMGLLFLTVPLLLVFSYVRIFWAVFVISSPGGRWKA
FSTCGSHLTVVLLFYGSLMGVYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLRNRDMKEALG
KLFVSGKTFEL (SEQ ID NO: 211)

ATGGAAGGTTTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACCAGGCAGA
GTGAACCAAACCACTGTTTCAGACTTCCTCCTTCTAGGACTCTCTGAGTGCCAGAGGAGC
AGCCTCTTCTGTTTGGCATCTTCCTTGGCATGTACCTGGTCACCATGGTGGGGAACCTGCTC
ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATACTCCCATGTACTTCTTTCTGGCCAA
30 CCTGTCAATTAAGTATGCCTGTTTCACTTCTGCCTCCATCCCCAAAATGCTGGCCAACATTC
ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGTCTTGCACAGCTATATTTCTCCTTATG
TTTGGTGGCCTTGACAACTGCCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT
GCCAACCACTCCATTACAGCACATCTATGAGTCCCCAGCTCTGTGCACTAATGCTGGGTGT
GTGCTGGGTGCTAACCAACTGTCCTGCCCTGATGCACACACTGTTGCTGACCCGCGTGGCT
35 TTCTGTGCCAGAAAGCCATCCCTCATTCTATTGTGATCCTAGTGCTCTCCTGAAGCTTGC
CTGCTCAGATACCCATGTAAACGAGCTGATGATCATCACCATGGGCTTGTGTTCTCCTCACT
GTTCCCTCCTGATCGTCTTCTCCTATGTCCGCATTTTCTGGGCTGTGTTTGTATCTC
ATCTCCTGGAGGGAGATGGAAGGCCTTCTCTACCTGTGGTTCTCATCTCACGGTGGTTCTG
CTCTTCTATGGGTCTCTTATGGGTGTGATTTACTTCCCTCCATCAACTTACTCTACAGAGAG
40 GGAAAGTAGGGCTGCTGTTCTCTATATGGTGATTATTTCCACGCTAAACCCATTATTTAT
AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAAACTTTTGTGAGTGGAACAAACA
TTCTTTTTATGA (SEQ ID NO: 212)

AOLFR116 sequences:

MDEANHSVSVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFLLAN
45 LSIINLVFCSSTAPKMIYDLFRKHKTIISFGGCVVQIFFIHAVGGTEMVLLIAMAFDRYVAICKPLH
YLTIMNPQRCILFLVISWIIHHSVIQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV
TANSGFISLASFLILISYIFILVTVQKKSSGGIFKAFSMLSAHVIVVVLVFGPLIFFYIFPFPTSHLD
KFLAIFDAVITPVLNPVIYTFRNKEMMVAMRRRCSQFVNYSKIF (SEQ ID NO: 213)

ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTTCTGGGACTCTCTGACTCGC
GGAAGATCCAGCTCCTCCTCTTCTCTTTTCTCAGTGTTCTATGTATCAAGCCTGATGGGA
AATCTCCTCATTGTGCTAACTGTGACCTCTGACCCTCGTTTACAGTCCCCCATGTACTTCT
GCTGGCCAACCTTCCATCATCAATTTGGTATTTTGTTCCTCCACAGCTCCCAAGATGATTT
55 ATGACCTTTTACAGGAAGCACAAAGACCATCTCTTTTGGGGGCTGTGTAGTTTACAGATCTTCT
TATCCATGCAGTTGGGGGAACCTGAGATGGTGCTGCTCATAGCCATGGCTTTTGACCGATAT

GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTTTGT
 TTTTAGTCATTTCCCTGGATTATAGGTATTATTCAGTCAGTGATTGAGTTGGCTTTTGTGTA
 GACCTGCTGTTCTGTGGCCCTAATGAATTAGATAGTTTCTTTTGTGATCTTCTCGATTTAT
 CAAACTGGCTTGCATAGAGACCTACACATTGGGATTTCATGGTTACTGCCAATAGTGGATTT
 5 ATTTCTCTGGCTTCTTTTTTAATTCTCATAATCTCTTACATCTTTATTTTGGTGACTGTTTCTCAG
 AAAAAATCTTCAGGTGGTATATTCAAGGCTTTCTCTATGCTGTCAGCTCATGTCATTGTGG
 TGGTTTTGGTCTTTGGGCCATTAATCTTTTTCTATATTTTCCATTTCCCACATCACATCTTG
 ATAAATTCTTGGCATCTTTGATGCAGTTATCACTCCCGTTTTGAATCCAGTCATCTATACT
 10 TTAGAAAATAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTAC
 AGTAAATCTTTTAA (SEQ ID NO: 214)

AOLFR117 sequences:

MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLLVISRLLLAMTLGNSTEVTEFYLLGFGA
 QHEFWCILFIVFLIYVTSIMGNSGILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSFT
 15 EEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPPYVAICKPLHYTVIMSRTVCIRLVAGSYI
 MGSINASVQTGFTCSLSFKSNSINHHFFCDVPPILALSCSNVDINIMLLVVFVGSNLIFTGLVVIFS
 YIYIMATILKMSSSAGRKKSFSTCASHLTAVTIFYGTL SYMYLQSHSNNSQENMKVAFIFYGTVI
 PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215)

20 ATGAATAACACTATTGTATTTGTCATAAAAAATACAAATAGAAAAAAGTGACTTGAAATATA
 GAGCCATTTTCATTGCAAGAAATCTCAAAGATTTCCCTTCTTTTCTGGGTCTTCTCTGGTC
 ATTTCTAGACTTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTCTATC
 TTCTGGGATTTGGTGCCAGCATGAGTTTTGGTGTATCCTCTTCATTGTATTCCTTCTCATC
 TATGTGACCTCCATAATGGGTAATAGTGAATAATCTTACTCATCAACACAGATTCCAGAT
 25 TTCAAACACTCACGTACTTTTTTCTACAACACTTTGGCTTTTGTGATATCTGTTACACTTCT
 GCTATCACTCCCAAGATGCTCCAAAGCTTCACAGAAGAAAAGAATTGATATTATTTTCAGG
 GCTGTGTGATACAATTCTTAGTTTATGCAACATTTGCAACCAGTGACTGTTATCTCTGGCT
 ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCCCTTCACTATACTGTAATCATGT
 CCCGAACAGTCTGCATCCGTTTGGTAGCTGGTTCATACATCATGGGCTCAATAAATGCCTC
 30 TGTACAAACAGTTTTACATGTTCACTGTCCTTCTGCAAGTCCAATAGCATCAATCACTTTT
 TCTGTGATGTTCCCCCTATTCTTGCTCTTTCATGCTCCAATGTTGACATCAACATCATGCTA
 CTTGTTGTCTTTGTGGGATCTAACTTGATATTCACTGGGTTGGTCGTCATCTTTTCTACAT
 CTACATCATGGCCACCATCCTGAAAATGTCTTCTAGTGCAGGAAGGAAAAAATCCTTCTCA
 ACATGTGCTTCCCACCTGACCGCAGTCACCATTTTCTATGGGACACTCTCTTACATGTATTT
 35 GCAGTCTCATTCTAATAATTCCCAGGAAAATATGAAAGTGGCCTTTATATTTTATGGCACA
 GTTATTCCCATGTTAAATCCTTTAATCTATAGCTTGAGAAAATAAGGAAGTAAAAGAAGCTT
 TAAAAGTGATAGGGAAAAAGTTATTTTAA (SEQ ID NO: 216)

AOLFR118 sequences:

40 MNHMSASLKISNSSKFQVSEFILLGFPGIHSWQHWLSLPLALLYLSALAANTLILIIWQNPSLQQ
 PMYIFLILCMVDMGLATTIIPKILAIWFDAKVISLPECFAQIYAIHFFVGMESGILLCMADFDRY
 VAICHPLRYPISVTSILKATLFMVLRNGLFVTPVPVLAQQRDYCSKNEIEHCLCSNLGVTSLA
 CDDRRPNSICQLVLAWLGMGSDLSLIILSYILILYSVLRNLNSAEAAAKALSTCSSHLTLILFFYTIV
 45 VVISVTHLTEMKATLIPVLLNVLHNIIPPSLNPTVYALQTKELRAAFQKVLFAITKEIRS (SEQ ID
 NO: 217)

ATGAATCATATGTCTGCATCTCTCAAAATCTCCAATAGCTCCAAATTCAGGTCTCTGAGTT
 CATCCTGCTGGGATTTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCCCTGGCA
 CTACTGTATCTCTCAGCACTTGCTGCAAAACACCCTCATCCTCATCATCTGGCAGAACCC
 50 TTCTTTACAGCAGCCCATGATATTTTCTTGGCATCCTCTGTATGGTAGACATGGGTCTGG
 CCACTACTATCATCCCTAAGATCCTGGCAACTCTTCTGGTTTGTATGCCAAGGTTATTAGCCTC
 CCTGAGTGCTTTGCTCAGATTTATGCCATTCACTCTTTGTGGGCATGGAGTCTGGTATCCT
 ACTCTGCATGGCTTTTGTAGATATGTGGCTATTTGTACCCTCTTCGCTATCCCATCAATTG
 TCACCAGTTCCTTAATCTTAAAGCTACCCTGTTTCATGGTGCTGAGAAATGGCTTATTTGTC
 55 ACTCCAGTGCCTGTGCTTGCAGCACAGCGTGATTATTGCTCCAAGAATGAAATTGAACACT
 GCCTGTGCTCTAACCTTGGGGTCACAAGCCTGGCTTGTGATGACAGGAGGCCAAACAGCAT

5 TTGCCAGTTGGTTCTGGCATGGCTTGGGAATGGGGAGTGATCTAAGTCTTATTATACTGTCA
TATATTTTGATTCTGTACTCTGTACTTAGACTGAACTCAGCTGAAGCTGCAGCCAAGGCC
TGAGCACTTGTAGTTCACATCTCACCTCATCTTTTCTTTTACACTATTGTTGTAGTGATT
TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATTCCAGTTCTACTTAATGTGTTGC
ACAACATCATCCCCCTTCCCTCAACCCTACAGTTTATGCACTTCAGACCAAAGAACTTAG
GGCAGCCTTCCAAAAGGTGCTGTTTGCCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:
218)

AOLFR119 sequences:

10 MPLFNSLCWFPTIHTVTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP
MYFFFGHALSLIDLLTCTTTLPNALCIFWFSLEKINFNACLAQMFFVHGFTGVESGVLMLMALD
RYIAICYPLRYATTLTNPIHAKAELATFLRGVLLMIPFPFLVKRLPFCQSNISHTYCDHMSVVKL
SCASIKVNVIIYGLMVALLIGVFDICCSLSYTLILKAAISLSSSDARQKAFSTCTAHISAIITYVPA
FPTFFAHRFGGHTIPPSLHIIVANLYLLPPTLNPIVYGVKTKQIRKSVIKFFQGDKGAG (SEQ ID
15 NO: 219)

20 ATGCCTCTATTTAATTCATTATGCTGGTTTCCAACAATTCATGTGACTCCTCCATCTTTTAT
TCTTAATGGAATACCTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCCACTCTGCACA
ATGTACATCATCTTCTTGTGGGGAATCTTGGTCTTGTGTACCTCATTATTATGAGGAGTC
CTTACATCATCCGATGATTTTTTTTTTGGCCATGCTCTCTCCCTCATTGACCTCCTTACCTG
CACCACCACTCTACCCAATGCACTCTGCATCTTCTGGTTCAGTCTCAAAGAAATTAACCTCA
ATGCTTGCTTGGCCCAGATGTTCTTTGTTTCATGGGTTACAGGTGTGGAGTCTGGGGTGTCT
CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCCTTTGCGTTATGCTACCACAC
25 TCACCAACCCTATCATTGCCAAGGCTGAGCTTGCCACCTTCTGAGGGGTGATTGCTGAT
GATTCTTTCCCATTTCTTGGTTAAGCGTTTGCCCTTTCTGCCAAAGCAATATTATCTCCATA
CGTACTGCGACCACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT
CTATGGTCTAATGGTTGCTCTCCTGATTGGAGTGTGTTGACATTTGTTGTATATCTTTGTCTT
ACACTTTGATCCTCAAGGCAGCGATCAGCCTCTCTTCATCAGATGCTCGGCAGAAGGCTTT
CAGCACCTGCACTGCCCATATATCTGCCATCATCATCACCTATGTTCCAGCATTCTTCACTT
30 TCTTTGCCACCGTTTTGGGGGACACACAATTCCCCCTTCTCTTCACATCATTGTGGCTAAT
CTTTATCTTCTTCTCCCCCAACTCTAAACCCTATTGTTTATGGAGTAAAGACAAAACAGAT
ACGCAAGAGTGTCTATAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGA (SEQ ID NO: 220)

AOLFR120 sequences:

35 MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENLAIIIIVVGLDHRLRRPMYF
FLTHLSCLEIWIYTSVTPKMLAGFIGVDGKNISYAGCLSQLFIFTFLGATECFLLAAMAYDRY
VAICMPLHYGAFVSWGTCIRLAAACWLVGFLTPILPIYLLSQLTFCGPNVIDHFSCDASPLLALS
CSDVTWKETVDFLVSLAVLLASSMVIASVGNIVWTLHIRSAAERWKAFSTCAHLTVVSLF
YGTLFFMYVQTKVTSSINFNKVVSVFYSVVTPLNPLIYSLRNKEVKALGRVFSLNFWKGQ
40 (SEQ ID NO: 221)

45 ATGCAACCATATACCAAAAACTGGACCCAGGTAACCTGAATTTGTCATGATGGGCTTTGCTG
GCATCCATGAAGCACACCTCCTCTTCTTCACTCTTCTCACCATGTACCTGTTACCTTG
GTGGAGAATTTGGCCATCATTTTATGTTGGGTTTGGACCACCGACTACGGAGACCCATGT
ATTTCTTCTGACACACTTGTCTGCCTTGAAATCTGGTACACTTCTGTTACAGTGCCCAAG
ATGCTGGCTGGTTTTATTGGGGTGGATGGTGGCAAGAATATCTCTTATGCTGGTTGCCTAT
CCCAGCTCTTCATCTTACCTTTCTTGGGGCAACTGAGTGTTCTCTACTGGCTGCCATGGCC
TATGATCGTTATGTGGCCATTTGTATGCCTCTCCACTATGGGGCTTTTGTGTCCTGGGGCAC
CTGCATCCGTCTGGCAGCTGCCTGTTGGCTGGTAGGTTTCTTACACCCATCTTGCCAATCT
50 ACCTCTTGTCTCAGCTAACATTTGTGGCCCAAATGTCATTGACCATTTCTCCTGTGATGCC
TCACCCTTGCTAGCCTTGTCGTGCTCAGATGTCACTTGAAGGAGACTGTGGATTTCCTGG
TGTCTCTGGCTGTGCTACTGGCCTCCTCTATGGTCACTTGTGCTGTCTATGGCAACATCGTC
TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCTTCTCTACCTATGTCAG
CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTTCTTTATGTATGTCCAGACCAAG
55 GTGACCTCCTCCATCAACTTCAACAAGGTGGTATCTGTCTTCTACTCTGTTGTCACGCCAT

GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTCGAGTC
TTTTCTCTCAACTTTTGGAAGGGACAGTGA (SEQ ID NO: 222)

AOLFR121 sequences:

5 MKRKNFTEVSEFIFLGFSSFGKHQITLFFVFLTVYILTLVANIIVTIIICIDHHLHTPMYFFLSMLA
SSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFFVILATNNCFLLTAMGYDRYVAICRPLRY
TVIMSKGLCAQLVCGSFGIGLTMAVLHVTAMFNLPCGTVDHFFCDIYPVMKLSCIDTTINEII
NYGVSSFVIFVPIGLIFISYVLVISSILQIASAEGRKKTATCVSHLTVVIVHCGCASIAYLKPKSES
SIEKDLVLSVTYTIITPLNPPVYSLRNKEVKDALCRVVGRNIS (SEQ ID NO: 223)

10 ATGAAGAGAGAAAGAACTTCACAGAAGTGTCAGAATTCATTTTCTTGGGATTTTCTAGCTTTG
GAAAGCATCAGATAACCCCTCTTGTGGTTTCTCTAACTGTCTACATTTTAACTCTGGTTGCT
AACATCATCATTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATTGTATTCTT
CCTAAGCATGCTGGCTAGTTCAGAGACGGTGTACACACTGGTCATTGTGCCACGAATGCCTT
15 TTGAGCCTCATTTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT
TTTTGTTATCTTGGCCACTAATAATTGCTTCCTGCTTACTGCAATGGGGTATGACCGCTATG
TGGCCATCTGCAGACCCCTGAGATACACTGTCATCATGAGCAAGGGACTATGTGCCAGCT
GGTGTGTGGGTCCTTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTTT
AATTGCGGTTCTGTGGCACAGTGGTAGACCACTTCTTTTGTGACATTTACCCAGTCATGA
20 AACTTTCTTGCAATTGATACCACTATCAATGAGATAATAAATTATGGTGTAAGTTCATTTGT
GATTTTGTGCCCATAGGCCTGATATTTATCTCCTATGTCCTTGTGATCTCTTCCATCCTTC
AAATTGCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGCTCCCCACCTCACTGT
GGTATTGTCCACTGTGGCTGTGCCTCCATTGCCTACCTCAAGCCGAAGTCAGAAAGTTCA
ATAGAAAAAGACCTTGTCTCTCAGTGACGTACACCATCATCACTCCCTTGCTGAACCCCTG
25 TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAA
ATATTTCTTAA (SEQ ID NO: 224)

AOLFR122 sequences:

30 MEWENQTLVEFFLKGHVSHPRELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTSIPSTLVSFLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMMAFDYVAICNPLR
YPIIMSKNAYVPMAGVSWFAGIVNSAVQTFVVLQPFCKRKNVINHFSCEILAVMKLACADISGN
EFLMLVATILFTLMPLLLVISYSLIISILKIHSSSEGRSKAFSTCSAHLTVVIIFYGTILFMYMKPKS
KETLNSDDLDATDKIISMFGVMTMPMNPLIYSLRNKDVKEAVKHLPNRRFFSK (SEQ ID NO:
225)

35 ATGGAATGGGAAAACCAAACCATTCTGGTGGAATTTTTTCTGAAGGGACATTCTGTTCCACC
CAAGGCTTGAGTTACTCTTTTTTGTGCTAATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTAATCAGCATCTTGGACCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACACTAG
40 TGAGCTTCCTTTCAGAAAGAAAGACCAATTTCTCTTTCTGGCTGTGCAGTGCAGATGTTCTT
GGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTATG
TGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGCAAGAATGCCTATGTACCCAT
GGCTGTTGGGTCCTGGTTTGCAGGGATTGTCAACTCTGCAGTACAACTACATTTGTAGTA
CAATTGCCTTTCTGCAGGAAGAATGTCATCAATCATTCTCATGTGAAATTCTAGCTGTCAT
45 GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCCTCATGCTTGTGGCCACAATATTG
TTCACATTGATGCCACTGCTCTTGATAGTTATCTTACTCATTAATCATTTCAGCATCCT
CAAGATTCACCTCTGAGGGGAGAAAGCAAGCTTTCTCTACCTGCTCAGCCCATCTGACT
GTGGTCATAATATTCTATGGGACCATCCTCTTCATGTATATGAAGCCCAAGTCTAAAGAGA
CACTTAATTCAGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTGAT
50 GACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCAGT
AAAACACCTACCGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 226)

AOLFR123 sequences:

55 MYRFTDFDVSNISIYLNHVLFYTTQQAGDLEHMETRNYSAMTEFFLVGLSQYPELQLFLFLCL
IMYMIILLGNSLLIITILDSRLHTPMYFFLGNL SFLDICYTSSSIPMLIIFMSERKSISFIGCALQM
VVSLLGLSTECVLLAVMAYDHYVAICNPLRYSIIMNGVLYVQMAAWSWIIGCLTSLQLTVLT

0986055_062201

MMLPFCGNNVIDHITCEILALLKLVCSDITINVLMITVTNIVSLVILLLLIFISYVFILSSILRINCAE
GRKKAFSTCSAHSIVILFYGSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPIIYSLRNKEV
KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

5 ATGTACAGATTTACAGATTTTGATGTATCAAACATTTCAATTTACCTGAATCATGTCCTTTT
CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT
GACTGAATTCTTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTTCTGTTCTCTGC
TCTGCCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCATTATCATCACCATC
TTGGATTCTCGCCTCCATACTCCCATGTATTTCTTTCTTGGAAACCTCTCATTCTTGGACAT
10 CTGTTACACATCCTCATCCATTCCTCCAATGCTTATTATATTTATGTCTGAGAGAAAAATCCA
TCTCCTTCATTGGCTGTGCTCTGCAGATGGTTGTGTCCCTTGGCTTGGGCTCCACTGAGTGT
GTCCTCCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCACTGAGGTACT
CCATCATCATGAACGGAGTGCTGTATGTGCAAATGGCTGCATGGTCTGGATCATAGGCTG
TCTGACCTCCCTATTGCAAACAGTTCTGACAATGATGTTGCCTTTCTGTGGGAATAATGTC
15 ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAACTTGTGTTGTTTCAGATATCACCAT
CAATGTGCTTATCATGACAGTGACAAATATTGTTTCACTGGTGATTCTTCTACTGTTAATTT
TCATCTCCTATGTGTTTATTCTCTCTTCCATCCTGAGAATTAATTGTGCTGAGGGAAGAAAG
AAAGCCTTCTCTACCTGTTTACGCGCACTCGATTGTGGTCATCTTATTCTACGGTTCAGCCCT
TTTTATGTACATGAAACCCAAGTCAAAGAACACTAATACATCTGATGAGATTATTGGGCTG
20 TCTTATGGAGTGGTAAGCCCAATGTTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG
TCAAAGAGGCTGTAAAGAAAGTCTGAGCAGACATCTGCATTTATTGAAAATGTGA (SEQ
ID NO: 228)

AOLFR124 sequences:

25 MNHSVVTEFIILGLTKKPELQGIIFLFLIVYLVAFLGNMLIIIAKIYNNTLHTPMYVFLTLAVV
DIICTTSIIPKMLGTMLTSENTISYAGCMSQLFLTWSLGAEMVLFTTMAYDRYVAICFPLHYST
VMNHHMCVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPLLALSCSPVRINEV
MVYVADITLAIGDFILTCISYGFIIIVAILRIRTVGKRFKAFSTCSSHLTVVTLYYSPVIYTYIRPASS
YTFERDKVVAALYTLVTPTLNPVVSFQNRMQAGIRKVF AFLKH (SEQ ID NO: 229)

30 ATGAATCACAGCGTTGTAACCTGAGTTCATTATTCTGGGCCTCACCAAAAAGCCTGAACTCC
AGGGAATTATCTTCCTCTTTTTTCTCATTGTCTATCTTGTGGCTTTTCTCGGCAACATGCTC
ATCATCATTGCCAAAATCTATAACAACACCTTGCATACGCCCATGTATGTTTTCTTCTGAC
ACTGGCTGTTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT
35 GCTAACATCAGAAAATACCATTTTCATATGCAGGCTGCATGTCCCAGCTCTTCTTGTTCACA
TGGTCTCTGGGAGCTGAGATGGTTCTCTTACCACCATGGCCTATGACCGCTATGTGGCCA
TTTGTCTCCCTCTTCATTACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC
ATGGTCATGGCTATTGCAGTCACCAATTCCTGGGTGCACACAGCTCTTATCATGAGGTTGA
CTTTCTGTGGGCCAAACACCATTGACCACTTCTTCTGTGAGATACCCCCATTGCTGGCTTTG
40 TCCTGTAGCCCTGTAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCCTGGCCA
TAGGGGACTTTATTCTTACCTGCATCTCCTATGGTTTTATCATTGTTGCTATTCTCCGTATC
CGCACAGTAGAAGGCAAGAGGAAGGCCTTCTCAACATGCTCATCTCATCTCACAGTGGTG
ACCTTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATTTGA
AAGAGACAAGGTGGTAGCTGCACTCTATACTCTTGTGACTCCACATTAAACCCGATGGTG
45 TACAGCTTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTTCTGAAA
CACTAG (SEQ ID NO: 230)

AOLFR125 sequences:

50 MTNQTQMMEFLLVRFTENWVLLRLHALLFSLIYLTAVLMNLVIIIIMILDHRLHMAMYFFLRH
LSFLDLCLISATVPKILNSVASTDSISFLGCVLQLFLVLLAGSEIGILTAMS YDRYAAICCP LHC
EAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSLNFYGSDELHQFFCDVPALLKLTC SKEHAI
ISVSVAIGVCYAFSCLVCIVVS YVYIFSAVLRISQRQRQSKAFSNCVPHLIVVTFLVTGAVAYL
KPGSDAPSILDLLVSVFYSVAPPTLNPVTYCLKNKDIKSALSKVLWNVRSSGVMKDD (SEQ ID
NO: 231)

55

ATGACCAATCAGACACAGATGATGGAATTCTTGCTTGTGAGATTTACTGAGAATTGGGTGC
TCCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATTTA
GTCATCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTTCTCCG
ACATTTGTCCTTCTTAGACCTGTGTCTCATTCTGCCACAGTCCCCAAATCCATCCTCAACT
5 CTGTCGCCTCCACTGACTCCATCTCCTTCTGGGGTGTGTGTTGCAGCTCTTCTTGGTGGTA
CTGCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCCTATGACCGCTATGCTGCCA
TCTGCTGCCCCCTACACTGTGAGGCTGTGATGAGCAGAGGGCTCTGTGTCCAGTTGATGGC
TCTGTCTGGCTCAACAGAGGGGCCCTTGGGACTCTTGTACACAGCTGGAACATTCTCTCG
AATTTTTATGGCTCTGATGAGCTACATCAGTTCTTCTGCGATGTCCCTGCCCTACTAAAGCT
10 CACTTGTCTTAAAGAACATGCCATCATTAGTGTGAGTGTGGCCATTGGGGTCTGTTATGCA
TTTTCATGTTTAGTTTGCATTGTAGTTTCTTATGTGTACATTTTCTCTGCTGTGTTAAGGAT
ATCACAGAGACAGAGACAATCCAAAGCCTTTTCCAAGTGTGTGCCTCACCTCATTGTTGTC
ACTGTGTTTCTTGTAAACAGGTGCTGTTGCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT
TCTAGACTTGCTGGTGTCTGTGTTCTATTCTGTGCGACCTCCAACCTTGAACCTGTTATCT
15 ACTGTCTGAAGAACAAGGACATTAAATCCGCTCTGAGTAAAGTCCTGTGGAATGTTAGAA
GCAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

AOLFR126 sequences:

MFLYLCFIFQRTCSEEMEEENATLLTEFVLTGFLHQPDKIPLFLAFLVIYLITIMGNLGLIVLIW
20 KDPHLHIPMYLFLGSLAFVDAISLSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL
ATMAYDRYVAICKALLYPVIMTNELCIQLLVLSFIGLLHALIHEAFSRLTFCNSNIIHFYCDII
PLLKISCTDSSINFLMVFIAGSVQVFTIGTILISYTHLFTILEKKSIRKAVSTCGAHLSSVSLY
YGPLTFKYLGSASPQADDQDMMESLFYTVIVPLLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID
NO: 233)

25 ATGTTCTCTTTACCTTTGCTTCATTTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA
ATGCAACATTGCTGACAGAGTTTGTCTCACAGGATTTTTACATCAACCTGACTGTAAAT
ACCGCTCTTCTGGCATTCTTGGTAATATATCTCATCACCATCATGGGGAATCTTGGTCTAA
TTGTTCTCATCTGAAAGACCTCACCTTCATATCCCAATGTACTTATTCCTTGGGAGTTTA
30 GCCTTTGTGGATGCTTCGTTATCATCCACAGTGACTCCGAAGATGCTGATCAACTTCTTAG
CTAAGAGTAAGATGATATCTCTCTCTGAATGCATGGTACAATTTTTTCCCTTGTAACCACT
GTAACCACAGAATGTTTTCTCTTGGCAACAATGGCATATGATCGCTATGTAGCCATTGCA
AAGCTTTACTTTATCCAGTCATTATGACCAATGAAGTATGCATTACAGCTATTAGTCTTGTCA
TTATAGGTGGCCTTCTTCATGCTTTAATCCATGAAGCTTTTTTCATTACAGATTACCTTCTG
35 TAATTCCAACATAATAACAACACTTTTACTGTGACATTATCCCATTGTTAAAGATTTCCTGTA
CTGATTCTCTATTAACTTTCTAATGGTTTTTATTTCGCAAGTTCTGTTCAAGTTTTTACCA
TTGGAACATTATCTTATATCTTATACAAATTATCTCTTTACAATCTTAGAAAAGAAGTCTATC
AAAGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTATACT
ATGGCCCCCTCACCTTCAAATATCTGGGCTCTGCATCTCCGCAAGCAGATGACCAAGATAT
40 GATGGAGTCTCTATTTTACACTGTCATAGTTCCTTTATTAATCCCATGATCTACAGCCTGA
GAAACAAGCAAGTAATAGCTTCATTACAAAAATGTTCAAAAGCAATGTTTAG (SEQ ID
NO: 234)

AOLFR127 sequences:

45 MSNEDMEQDNTLLTEFVLTGLTYQPEWKMPFLVFLVIYLITIVWNLGLIALIWNDPQLHIPM
YFFLGSLAFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQFFSFAFGGTTECFLLATMAYDRY
VAICKPLLYPVIMNNSLCIRLLAFSFLGGFLHALIHEVLIFRLTFCNSNIIHHFYCDIIPLMISCTD
PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLSSVSLYYGPLIF
MYLRPASQADDQDMIDSVFYTHIPLLNPIIYSLRNKQVIDSFTKMVKRNV (SEQ ID NO: 235)
50 ATGTCGAATGAGGACATGGAACAGGATAATACAACATTGCTGACAGAGTTTGTCTCACA
GGACTTACATATCAGCCAGAGTGGAAGATGCCCTGTTCTTGGTGTTCTTGGTGATCTATC
TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGGAATGACCCACAACCTCAC
ATCCCCATGTACTTTTTTCTTGGGAGTTTAGCCTTTGTTGATGCTTGGATATCTTCCACAGT
55 AACTCCCCAAATGTTGGTTAATTTCTTGGCCAAAAACAGGATGATATCTCTGTCTGAATGC
ATGATTCAATTTTTTCTTTGCATTGGTGGAACTACAGAATGTTTTCTTGGCAACAAT

GGCATATGATCGCTATGTAGCCATATGCAAACCTTTACTATATCCAGTGATTATGAACAAT
TCACTATGCATACGGCTGTTAGCCTTCTCATTCTTTAGGTGGCTTCCTCCATGCCTTAATTCA
TGAAGTCCTTATATTCAGATTAACCTTCTGCAATTCTAACATAATACATCATTCTTTACTGTG
ATATTATACCACTGTTTATGATTTCTGTACTGACCCTTCTATTAATTTTCTAATGGTTTTTA
5 TTTTGTCTGGCTCAATTCAGGTATTCACCATTGTGACAGTTCTTAATTCTTACACATTTGCT
CTTTTCACAATCCTAAAAAAGAAGTCTGTTAGAGGCGTAAGGAAAGCCTTTTCCACCTGTG
GAGCCCATCTCTTATCTGTCTCTTTATATTATGGCCCACTTATCTTCATGTATTTGCGCCCT
GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTTATACAATCATAATTC
CTTTGCTAAATCCCATATCTACAGTCTGAGAAATAACAAGTAATAGATTCATTACAAA
10 AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

AOLFR128 sequences:

METQNLTVVTEFILLGLTQSQDAQLLVFVLVLIFYLILPGNFLIIFTIKSDPGLTAPLYFFLGNLA
LLDASYSFIVPRMLVDFLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVMFAFDRIYAICRPLHY
15 STIMNPRACYALSLVLWLGFIHSIVQVALILHLPFCGPNQLDNFFCDVPQVIKLACTNTFVVEL
LMVSNSSLGSLLCFLGLLASYAVILCRIREHSSEGKSKAISTCTTHIIIFLMFGPAIFIYTCPFQAF
ADKVVSFLFHTVIFPLMNPVIYTLRNQEVKASMRKLLSQHMFC (SEQ ID NO: 237)

ATGGAAACACAGAACCTCACAGTGGTGACAGAATTCATTCTTCTTGGTCTGACCCAGTCTC
20 AAGATGCTCAACTTCTGGTCTTTGTGCTAGTCTTAATTTTCTACCTTATCATCCTCCCTGGA
AATTTCTCATCATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCTT
TCTGGGCAACTTGGCCTTACTGGATGCATCCTACTCCTTCAATTGTGGTTCCAGGATTTG
GTGGACTTCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTAGCTCTTTT
TCTTGCAATTTCTTGGAGCGGGAGAGATGTTCTCCTCCTCGTTGTGATGGCCTTTGACCGCTAC
25 ATCGCCATCTGCCGCCCTTTACACTATTCAACCATCATGAACCCTAGAGCCTGCTATGCAT
TATCGTTGGTTCTGTGGCTTGGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG
CACTTGCCTTTCTGTGGCCCAAACCAGCTCGATAACTTCTTCTGTGATGTTCCACAGGTCAT
CAAGCTGGCCTGCACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCCAACAGTGGCCTG
CTCAGCCTCCTGTGCTTCTTGGCCTTCTGGCCTCCTATGCAGTCATCCTCTGTCTGATAAG
30 GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCCACATGCACCACCCATATTATCATT
ATATTTCTCATGTTTGGACCTGCTATTTTCATCTACACTTGCCCCCTCCAGGCTTTCCAGC
TGACAAGGTAGTTTCTCTTTCCATACTGTCATCTTTCTTTGATGAACCCTGTTATTTATA
CGCTTCGCAACCAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTTG
CTGA (SEQ ID NO: 238)

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AOLFR129 sequences:

MALYFSLILHGMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLLFALFSVI
YVVTVLGNLLIIVTFVNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT
QIFLLHLLGGVEMVLLVSMFAFDRIYAICKPLHYMTIMNKKVCVLLVVTSWLLGLLHSGFQIPF
40 AVNLPFCGPNVVDISFCDLPLVTKLACIDIYFVQVVIVANSGLSLSCFIILLISYSLILITIKNHSPT
GQSKARSTLTAHITVVILFFGPCIFIYIWPFGNHSVDKFLAVFYTIITPILNPIIYTLRNKEMKISMK
KLWRAFNVSREDT (SEQ ID NO: 239)

ATGGCTCTTTATTTTTCACCTCATACTCCATGGTATGAGTGATCTTTTCTTTCTCTCTACAGG
45 TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAACTATTAAATCAATCTCAAGTGTC
AGAATTCATTTTGTGGGACTGACCAGCTCCCAGGATGTAGAGTTTCTTCTTTGCCCTCT
TCTCGGTTATCTATGTGGTCACAGTTTTGGGTAACCTTCTTATTATAGTCACAGTGTTAAC
ACCCCTAACCTGAATACTCCCATGTATTTTCTCCTTGGTAATCTCTCTTTGTAGATATGAC
CCTTGCTTCTTTTGCCACCCCTAAGGTGATTCTGAACCTGTGTAAGGAGCAGAGGTAATT
50 TCTTTTGTGCTGGGTGCTTCACTCAGATATTTCTCCTTCACTTACTGGGTGGGGTTGAAATGGT
ACTGTTGGTCTCCATGGCTTTTGACAGATATGTGGCCATTTGTAAGCCCTACACTACATG
ACCATCATGAACAAGAAGGTATGTGTTTTGCTTGTAGTGACCTCATGGCTCTTGGGTCTCC
TTCACCTAGGGTTTCAGATACCATTGCTGTGAACCTTGCCCTTTTGTGGTCCCAATGTGGTA
GACAGCATTTTTTGTGACCTCCCTTTGGTTACTAAGCTTGCCCTGTATAGACATATATTTTGT
55 ACAGGTAGTCATTGTTGCCAACAGTGGCATAATCTCCCTGAGCTGTTTCATTATTTTGTCTTA
TCTCCTACAGTCTGATCCTCATAACCATTAAAGAACCACTCTCCTACTGGGCAATCTAAAGC

CCGTTCCACTTTGACTGCTCACATCACAGTGGTGATTCTCTTCTTTGGCCCATGCATCTTTA
TCTACATTTGGCCCTTCGGCAACCACTCTGTAGATAAGTTCCTTGCTGTGTTTTATACCATC
ATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACAAAGAAATGAAGATATCCA
TGAAAAAACTCTGGAGAGCTTTTGTGAATTCTAGAGAAGATACTTAG (SEQ ID NO: 240)

5

AOLFR131 sequences:

MASTSNVTELIIFTGLFQDPAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS
LVEISYSSTIAPKFIIDLLAKIKTISLEGCLTQIFFHFFGVAEILLIVVMAYDCYVAICKPLHYMNI
ISRQLCHLLVAGSWLGGFCHSIIQILVIIQLPFCGPNVIDHYFCDLQPLFKLACTDTFMEGVIVLA
NSGLFSVFSFLILVSSYIVLVNLRNHSAGEGRHKALSTCASHITVVILFFGPAIFLYMRPSSTFTED
KLVAVFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)

10

ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG
TGCAGAGTGATGCTTTGTGGTGTTTCTCCCCGTGTACCTTGCCACGGTGGTGGGCAATGG
CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTTCCTTA
GCTGCCTGTCCTTGGTGGAGATCAGTTATTCTCCACTATCGCCCCTAAATTCATCATAGAC
TTACTTGCCAAGATTAACCAATCTCTCTGGAAGGCTGTCTGACTCAGATATTCTTCTTCCA
CTTCTTTGGGGTTGCTGAGATCCTTTTGATTGTGGTGATGGCCTATGATTGCTACGTGGCC
ATTTGCAAGCCTCTTCATTATATGAACATTATCAGTCGTCAACTGTGTACCTTCTGGTGGC
TGGTTCCTGGCTGGGGGGCTTTTGTCACTCCATAATTCAGATTCTCGTTATCATCCAATTGC
CCTTCTGTGGTCCCAATGTGATTGACCACTATTTCTGTGACCTCCAGCCTTTATTCAAGCTT
GCCTGCACTGACACCTTCATGGAGGGGGTTATTGTGTTGGCCAACAGTGGATTATTCTCTG
TCTTCTCCTTCCTCATCTTGGTGTCTCTTATATTGTCATTCTGGTCAACTTGAGGAACCAT
TCTGCAGAGGGGAGGCACAAAGCCCTCTCCACCTGTGCTTCTCACATCACAGTGGTCATCT
TGTTTTTGGACCTGCTATCTTCTCTACATGCGACCTTCTTCCACTTTCAGTGAAGATAAA
CTTGTGGCTGTATTCTACACGGTCATCACCCCATGCTGAACCCCATCATTTACACACTCAG
GAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGGA
GGGAGTGA (SEQ ID NO: 242)

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AOLFR132 sequences:

MVATNNVTEIIFVGFSQNWSEQRVISVMFLLMYTAVVLGNGLIVVTILASKVLTSPMYFFLSYL
SFVEICYCSVMAPKLIFDSFIKRKVISLKGCLTQMFSLHFFGGTEAFLLMVMAYDRYVAICKPL
HYMAIMNQRMCGLLVRIAWGGGGLLSVGGTFLIFQLPFCGPNIMDHYFCDVHPVLELACADT
FFISLLIITNGGSISVVSFFVLMA SYLILHFLRSHNLEGQHKALSTCASHVTVDLFFPCSLVYIR
PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

35

ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCCAGAATTGGAGTG
AGCAGAGGGTGATTTCTGTGATGTTTCTCCTCATGTACACAGCTGTTGTGCTGGGCAATGG
CCTCATTGTGGTGACCATCCTGGCCAGCAAAGTGCTCACCTCCCCATGTATTTCTTTCTCA
GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTATGGCCCCCAAGCTTATCTTTGAC
TCCTTTATCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTTCCCTCC
ATTTCTTTGGTGGCACTGAGGCCCTTCTCCTGATGGTGATGGCCTATGACCGCTATGTGGC
CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAGCGAATGTGTGGTCTCCTCGTG
AGGATAGCATGGGGCGGGGGCCTGCTGCATTCTGTTGGGCAAACCTTCTGATTTTCCAGC
TCCCGTTCTGTGGCCCCAACATCATGGACCACTACTTCTGTGATGTCCACCCAGTGCTGGA
GCTGGCCTGCGCAGACACCTTCTTATTAGCCTGCTGATCATCACCATGGCGGCTCCATC
TCCGTAGTCAGTTTCTCGTGCTGATGGCTTCTACCTGATCATCCTGCACTTCTGAGAAG
CCACAACCTTGGAGGGGAGCACAAGGCCCTCTCCACCTGTGCCTCTCATGTACAGTTGTC
GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTACCCTCCCTGCAGA
CAAGATAGTTGCTGTATTTTATACAGTGGTCACACCTCTCTTAAACCCTGTGATTTACTCCT
TCAGGAATGCTGAAGTGAAAATGCCATGAGGAGATTATTGGGGGAAAAGTAATTGA
(SEQ ID NO: 244)

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AOLFR133 sequences:

MTEFIFLVLSPNQEVQRVCFVIFLFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS
SATAPKLISDLLAERKVISWWGCMALFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN

55

WQVCTVLVGIAWVGGMHSAQILLIFHLLFCGPNVINHYFCDLVPLLKLACSDTFLLIGLLIVAN
GGTLSVISFGVLLASYMVILLHLRTWSSEGWCKALSTCGSHFAVVILFFGPCVFNSLRPSTTLPI
DKMVAVFYTVITAILNPVIYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

5 ATGACTGAATTCATTTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG
TGATATTTCTGTTCTTGTACACAGCAATTGTGCTGGGGAATTCCTCATTGTGCTCACTGTC
ATGACCAGCAGAAGCCTTGGTTCCCCCATGTACTTCTTCCTCAGCTACCTCTCCTTCATGGA
GATCTGCTACTCCTCCGCTACAGCCCCCAAACATCTCAGATCTGCTGGCTGAAAGGAAA
GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTTCTTGCCTTCTTTGGTGGCACTGA
10 GATTTTCTGCTCACTGTGATGGCCTATGACCACTATGTGGCCATCTGCAAGCCCCTCAGC
TACACCACCATCATGAACCTGGCAGGTGTGTACTGTCCTTGTAGGAATAGCATGGGTGGGA
GGCTTCATGCATTCTTTGCACAAATCCTTCTCATCTTCCACCTGCTCTTCTGTGGCCCCAA
TGTGATCAATCACTATTTCTGTGACCTAGTTCCCCCTTCTCAAACCTGCCTGCTCTGACACCT
15 TCCTCATTGGTCTGCTGATTGTTGCCAATGGAGGCACCCTGTCTGTGATCAGTTTGGGGT
CCTCTTAGCATCCTATATGGTCATCTTGTCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG
TGCAAGCCCCTCTCCACCTGTGGGTCCCATTTCGCTGTGGTTATCTTGTCTTTGGGCCCTG
CGTCTTCAACTCTTGAGGCCTTCTACCCTCTGCCCATAGACAAGATGGTGGCTGTGTTCT
ACACAGTGATAACCGCGATCCTGAACCTGTCTACTCTCTGAGAAATGCTGAAATGAG
GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID
20 NO: 246)

AOLFR134 sequences:

MTTILEVDNHTVTTRFILLGFPTRP AFQLFFSIFLATYLLTLENLLIILAIHSDGQLHKPMYFFL
SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC
25 NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFIQLHYCGMPQINHYFCDISPLLNVSC
DASQAEMVDFFLALMVIAIPLCVVVASYAAILATILRIPSAQGRQKAFSTCASHLTVVILFYSMT
LFTYARPKLMYAYNSNKVSVLYTVIVPLLNPIHYCLRNHEVKAALRKTIHCRGSGPQGN GAFS
S (SEQ ID NO: 247)

30 ATGACCACCATAATTCTGGAAGTAGATAATCATACAGTGACAACACGTTTTATTCTTCTGG
GGTTTCCAACACGACCAGCCTTCCAGCTTCTCTTTTTCTCCATTTTCCTGGCAACCTATCTG
CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA
AGCCCATGTACTTCTTCTTGAGCCACCTCTCCTTCTGGAGATGTGGTATGTCACAGTCATC
AGCCCCAAGATGCTTGTGACTTCCTCAGTCATGACAAGAGTATTTCTTCAATGGCTGCA
35 TGACTCAACTTTACTTTTTTGTGACCTTGTCTGCACTGAGTACATCCTTCTTGCTATCATG
GCCTTTGACCGCTATGTAGCCATTTGTAATCCACTACGCTACCCAGTCATCATGACCAACC
AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTTCTGTGGACTCATGACTGCCATGATTAA
GATGGTTTTTATAGCACAACCTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTGTG
ATATCTCTCCACTCCTTAACGTCTCCTGTGAGGATGCCTCACAGGCTGAGATGGTGGACTT
40 CTTCTTGGCCCTCATGGTCATTGCTATTCTCTTTGTGTTGTGGTGGCATCCTACGCTGCTA
TCCTTGCCACCATCCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTCTCCACCTG
TGCTCCCACCTGACCGTCGTAATTCTCTTCTATTCCATGACACTTTTACCTATGCCCCGTC
CCAAACTCATGTATGCCTACAATTCCAACAAAGTGGTATCTGTTCTCTACACTGTCAATTGTT
CCTCTCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA
45 AGACCATACATTGCAGAGGAAGTGGGCCCCAGGGAAATGGGGCTTTCAGTAGTTAA (SEQ
ID NO: 248)

AOLFR135 sequences:

MIFPSHDSQAFTSVDMEVGNTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILIRT
50 DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL
AAMAYDRHAAICNPILYSGTMSTALCTGLVAGSYIGGFLNAIAHTANTFRLHFCGKNIDHFFC
DAPPLVKMSCTNTRVYEKVLG VVGFTVLSSILAILISYVNILLAILRIHSASGRHKAFSTCASHL
ISVMLFYGSLLFMYSRPSSTYSLERDKVAALFYTVINPLLNPLIYSLRNKDIKEAFRKATQTIQPQ
T (SEQ ID NO: 249)

55

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTCACCTCCGTGGACATGGAAGTGGGAAATT
GCACCATCCTGACTGAATTCATCTTGTGGGTTTCTCAGCAGATTCCCAGTGGCAGCCGAT
TCTATTTGGAGTGTCTCTGATGCTCTATTTGATAACCTTGTGAGGAAACATGACCTTGGTTA
TCTTAATCCGAAGTATTCCCACTTGCATACACCTATGTACTTTTTCATTGGCAATCTGTCT
5 TTTTGGATTCTGGTATACCTCTGTGTATACCCCAAAATCCTGGCCAGTTGTGTCTCAGA
AGATAAGCGCATTTTCTTGGCTGGATGTGGGGCTCAGCTGTTTTTTTCTGTGTGTAGCCT
ACACTGAATGCTATCTCCTGGCAGCCATGGCATATGACCGCCATGCAGCAATTTGTAACCC
ATTGCTTTATTACAGGTACCATGTCCACCGCCCTCTGTACTGGGCTTGTGCTGGCTCCTACA
TAGGAGGATTTTGAATGCCATAGCCCATACTGCCAATACATTCCGCCTGCATTTTGTGG
10 TAAAAATATCATTGACCACTTTTCTGTGATGCACCACCATTTGGTAAAAATGTCCTGTACA
AACACCGGGTCTACGAAAAAGTCCTGCTTGGTGTGGTGGGCTTACAGTACTCTCCAGCA
TTCTTGCTATCTGATTTCCTATGTCAACATCCTCCTGGCTATCCTGAGAATCCACTCAGCT
TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCCACCTCATCTCAGTCATGCTCTTCTA
TGGATCATTGTTGTTTATGTATTCAAGGCCTAGTTCCACCTACTCCCTAGAGAGGGGACAAA
15 GTAGCTGCTCTGTTCTACACCGTGATCAACCCACTGCTCAACCCTCTCATCTATAGCCTGAG
AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG
A (SEQ ID NO: 250)

AOLFR136 sequences:

20 MTMENYSMAAQFVLDGLTQQAELQLPLFLFLGIYVTVVGNLGMILLIAVSPLLHTPMYYFL
SSLSFVDFCYSSVITPKMLVNFLGKKNLILYSECMVQLFFFVVFVVAEGYLLTAMAYDRYVAIC
SPLLYNAIMSSWVCSLLVLAFFLGLSALHTSMMKLSFCKSHIINHYFCDVLPNLSNCSNT
HLNELLFHAGFNTLVPTLAVAVSYAFILYSILHIRSSEGRSKAFGTCSSHLMAVVIFFGSITFMY
FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)

25 ATGACCATGGAATAATTCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAACACAGCAAG
CAGAGCTCCAGCTGCCCCCTCTTCTCCTGTTTCTGGGAATCTATGTGGTCACAGTAGTGGG
CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTCTACTTCACACCCCCATGTACTATT
TCCTCAGCAGCTTGTCTTCTGTCGATTCTGCTATTCTCTGTCTACTCCCAAAATGCTG
30 GTGAATTCCTAGGAAAGAAGAATACAATCCTTTACTCTGAGTGCATGGTCCAGCTCTTT
TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCCTGACTGCCATGGCATATGATCGCTA
TGTTGCCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCTCATGGGTCTGCTCACTGC
TAGTGCTGGCTGCCTTCTTCTTGGGCTTTCTCTCTGCCTTGACTCATACAAGTGCCATGATG
AAACTGTCTTTTGCAAATCCACATTATCAACCATTACTTCTGTGATGTTCTTCCCCCTCT
35 CAATCTCTCCTGCTCCAACACACACCTCAATGAGCTTCTACTTTTATCATTGCGGGGTTTA
ACACCTTGGTGCCCAACCTAGCTGTTGCTGTCTCCTATGCCTTCATCCTCTACAGCATCCTT
CACATCCGCTCCTCAGAGGGCCGGTCCAAAGCTTTTGGAACATGCAGCTCTCATCTCATGG
CTGTGGTGATCTTCTTGGGTCCATTACCTTCATGTATTTCAAGCCCCCTTCAAGTAACTCC
CTGGACCAGGAGAAGGTGTCCTCTGTGTTCTACACCACGGTGATCCCCATGCTGAACCCTT
40 TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAAGGAAGGTCTTAGTAGGAA
AATGA (SEQ ID NO: 252)

AOLFR137 sequences:

45 MSPENQSSVSEFLLGLPIRPEQQAFFALFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
LALTDISFSSVTPKMLNMQTOHLAVFYKGCISQTYFFIFFADLDSFLITSMAYDRYVAICHPL
HYATIMTQSQCVM LVAGSWVIACACALLHTLLLAQLSFCADHIIPHYFCDLGALLKLSCSDTSL
NQLAIFTAALTAIMLPFLCILVSYGHIGVTILQIPSTKGICKALSTCGSHLSVVTIYYRTIIGLYFLP
PSSNTNDKNIIASVIYTA VTPMLNPFYISLRNKDIKGALRKLLSRGAVAHACNLSTLGG (SEQ
ID NO: 253)

50 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTCCTGGGCCTCCCCATCCGGC
CAGAGCAGCAGGCCGTGTTCTTCGCCCTGTTCTGCGGCATGTACCTGACCACGGTGCTGGG
GAACCTGCTCATCATGCTGCTCATCCAGCTAGACTCTCACCTTCACACCCCCATGTACTTCT
TCCTTAGCCACTTGGCCCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
55 ATGAACATGCAGACTCAGCACCTAGCCGTCTTTTACAAGGGATGCATTTACAGACATATT
TTTTCATATTTTGTGACTTAGACAGTTTCTTATCACTTCAATGGCATATGACAGGTAT

GTGGCCATCTGTCATCCTCTACATTATGCCACCATCATGACTCAGAGCCAGTGTGTCATGC
TGGTGGCTGGGTCCCTGGGTCATCGCTTGTGCGTGTGCTCTTTTGCATACCCCTCCTGGCC
CAGCTTTCCTTCTGTGCTGACCACATCATCCCTCACTACTTCTGTGACCTTGGTGGCCTGCT
CAAGTTGTCCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA
5 GCCATTATGCTTCCATTCTGTGCATCCTGGTTTCTTATGGTCACATTGGGGTCACCATCCT
CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTTGTCCACTTGTGGATCCCACCTCTCA
GTGGTGACTATCTATTATCGGACAATTATTGGTCTCTATTTTCTTCCCCCATCCAGCAACAC
CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA
TTCATTACAGTCTGAGAAATAAAGACATTAAGGGAGCCCTAAGAAAACTCTTGAGTAGG
10 TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

AOLFR138 sequences:

MLNFTDVTEFILLGLTSRREWQVLFVFLVYIITVVGNIGMMLLIKVSPQLNSPMYFFLSHLS
FVDVWFSSNVTPKMLENLFSDDKKTISYADCLAQCFFIALVHVEIFILAAIAFDRTVIGNPLLY
15 GSKMSRGVCIRLITFPYIYGFLTSLTATLWYGLYFCGKIEINHFCADPPLIKMACAGTFVKEY
TMLILAGNFTYSLTVIISYLFILAILRMRSAEGRQKAFSTCGSHPTAVIIFYGTLIFMYLRRPTE
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

ATGCTCAATTTACCCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGGGAAT
20 GGCAAGTTCTCTTCTTCATCGTTTTTCTGTGGTCTACATTATCACCGTGGTGGGCAATATC
GGCATGATGTTGTTAATCAAGGTCAGTCCTCAGCTTAACAGCCCCATGTACTTTTCTCTCA
GTCATTGTCAATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAATAAT
CTGTTATCAGATAAAAAACAATTTCTTATGCTGGCTGTTTAGCACAGTGTCTTCTTCTCAT
TGCTCTTGTCCATGTGGAATTTTATTCTTGCTGCGATTGCCTTTGATAGATACACAGTGA
25 TTGGAATCCCTTTGCTTTATGGCAGCAAAATGTCAAGGGATGTCTGTATTTCGACTGATTAC
TTCCCTTACATTTATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTTGT
ACTTCTGTGAAAAAATTGAGATCAACCATTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGCTCATACTTGCCGGCATCAACTTC
ACATATTCCTGACTGTAATTATCATCTCTTACTTATTATCATCCTCATTGCCATTCTGCGAAT
30 GCGCTCAGCAGAAGGAAGGCAGAAAGGCCTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATCATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTAA (SEQ ID NO: 256)

35

AOLFR139 sequences:

MGFPGIHSWQHWSLPLALLYLLALSANILILIINKEAALHQPMMYYFLGILAMADIGLATTIMP
KILAILWFNAKTISLLECFAQMYAIHCFVAMESSTFVCMAIDRYVAICRPLRPSIITESFVFKAN
GFMALRNSLCLISVPLLAQRHYCSQNQIEHCLCSNLGVTSLSCDDRRINSINQVLLAWTLMGS
40 DLGLILSYALILYSVLKLNPEAASKALSTCTSHLILILFFYTVIIVISITRSTGMRVPLIPVLLNL
HNVIPPALNPMVYALKNKELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCCTGGCTCTGCTCT
ACCTCTTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGCAGCACT
45 GCACCAGCCTATGTACTATTTCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTACC
ACCATCATGCCTAAGATTTTGGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG
AGTGCTTTGCTCAGATGTATGCCATACATTGCTTTGTGGCCATGGAATCAAGTACCTTTGT
CTGCATGGCTATTGATAGATATGTAGCCATTTGTGACCGCTACGATATCCATCAATCATC
ACTGAATCTTTTGTTCCTTCAAAGCAAATGGGTTTCATGGCACTGAGAAACAGCCTGTGTCTCA
50 TCTCAGTGCCTCTGTTGGCTGCCAGAGGCATTACTGCTCCAGAAATCAAATTGAGCACTG
TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCATT
AACCAGGTCTTTTGGCTTGGACACTCATGGGAAGTGACCTGGGTTTGATTATTTTATCAT
ATGCTCTAATACTTTACTCTGTCTGAAGCTGAACTCTCCAGAAGCTGCATCCAAGGCCTT
AAGTACCTGCACCTCCCACCTCATCTTAATCCTTTTCTTCTACACAGTCATCATTGTGATTT
55 CCATTACTCGTAGTACAGGAATGAGAGTTCCTTATTCCAGTTCTACTTAATGTGCTACA

CAATGTCATTCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAGGAACTCAGG
CAAGGCTTATACAAGGTACTTAGACTGGGAGTGAAGGGCACCTGA (SEQ ID NO: 258)

AOLFR140 sequences:

5 MLTLNKTDLIPASFILNGVPGLEDQLWISFPFCSMYVAMVGNCGLLYLIHYEDALHKPMYV
FLAMLSFTDLVMCSSTIPKALCIFWFHLKDIGFDECLVQMFFIHTFTGMESGVLMMLALDRYV
AICYPLRYSTILTNPVIAKVGTATFLRGVLLIIPFTFLTKRLPYCRGNILPHTYCDHMSVAKLSCG
NVKVNAIYGLMVALLIGGFDILCITISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAF
10 FSFFSHRFGHEIIPPSCHIIIVANIYLLLPPTMNPVYGVKTKQIRDCVIRILSGSKDTKSYSM (SEQ
ID NO: 259)

ATGCTAACTGAATAAAACAGACCTAATACCAGCTTCATTTATTCTGAATGGAGTCCCAG
GACTGGAAGACACAACTCTGGATTTCCCTTCCCATTCTGCTCTATGTATGTTGTGGCTAT
GGTAGGGAATTGTGGACTCCTTACTTACTTACTGACCTTGTTATGTGCTCTAGTACAATCCCATA
15 TACTACTTCTTGGCCATGCTTTCCTTTACTGACCTTGTTATGTGCTCTAGTACAATCCCATA
AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTTGATGAATGCCTTGTCCAG
ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGCTTATGCTTATGGCCCTGG
ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTCACCAATCCTGTAATT
GCAAAGGTTGGGACTGCCACCTTCCTGAGAGGGGTATTACTCATTATTCCCTTTACTTTTCT
20 CACCAAGCGCCTGCCCTACTGCAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG
TCTGTAGCCAAATTGTCCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG
CCCTCCTGATTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCTCCGG
GCAGTGGTCAGCCTCTCCTCAGCAGATGCTCGGCAGAAAGGCCTTTAATACCTGCACTGCCC
ACATTTGTGCCATTGTTTTCTCTATACTCCAGCTTTCTTCTCCTTCTTTTCCCACCGCTTTG
25 GGGAACACATAATCCCCCTTCTTGCCACATCATTGTAGCCAATATTATCTGCTCCTACCA
CCCACTATGAACCCTATTGTCTATGGGGTGAAAACCAACAGATACGAGACTGTGTCATAA
GGATCCTTTCAGGTTCTAAGGATACCAATCCTACAGCATGTGA (SEQ ID NO: 260)

AOLFR141 sequences:

30 MSSTLGHNMESPNHTDVPDPSVFLLGIPGLEQFHLWLSLPVCGLTATIVGNITILVVVATEPVL
HKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHAFMCMESTVLLAM
AFDRYVAICHPLRYATILDTIIAHIGVAAVVRGSLMLPCPFLIGRLNFCQSHVILHTYCEHMA
VVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVC
VILISYTPALFSFFTHRFHGHVPVHIHILLANVYLLPPALNPVVYGVKTKQIRKRVVRVFQSGQ
35 GMGIKASE (SEQ ID NO: 261)

ATGTCCAGCACTCTTGGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCTTCTG
TCTTCTTCTCCTGCGCATCCCAGGTCTGGAACAATTTCAATTTGTGGCTCTCACTCCCTGTG
TGTGGCTTAGGCACAGCCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTG
40 AACCAGTCTTGACAAGCCTGTGTACCTTTTCTGTGCATGCTCTCAACCATCGACTTGGCT
GCCTCTGTCTCCACAGTTCCTCAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT
CTGCCTCTGCCTGCCTGGCACAGATGTTCTTCATTCATGCCTTCTGCATGATGGAGTCCACT
GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA
CAATCCTCACTGACACCATCATTGCCACATAGGGGTGGCAGCTGTAGTGCAGGGTCCCT
45 GCTCATGCTCCCATGTCCCTTCCTTATTGGGCGTTTGAACCTTCTGCCAAAGCCATGTGATCC
TACACACGTACTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGAGACACCAGGCCTA
ACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCATTGGGGTTGACTTGTTTTGCATTGG
TCTCTCCTATGCCCTAAGTGACAAGCTGTCTTTCGCTCTCATCCCATGAAGCTCGGTCCA
AGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTCATCCTCATCTCTTATACACCAGCCCTC
50 TTCTCCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTACATTCTTTTGGC
CAATGTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAAAC
AGATCCGTAAAAGAGTTGTCAGGGTGTTTCAAAGTGGGCAGGGAATGGGCATCAAGGCAT
CTGAGTGA (SEQ ID NO: 262)

55

AOLFR143 sequences:

MLGLNGTPFQPATLQLTGIPGIQTGLTWVALIFCILYMISIVGNLSILTLVFWEPALHQPMMYYFL
SMLALNDLGVSFSTLPTVISTFCFNYNHVAFNACLVQMFFIHTFSFMESGILLAMSLDRFVAICY
PLRYVTVLTHNRILAMGLILTKSFTTLFPFPFVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI
5 HVNNIYGLLVIIIFTYGMDSFTILLSYALILRAMLVHSQEQRLKALNTCMSHICAVLAFYVPIIAVS
MIHRFWKSAPPVVHVMMNSNVYLFVPPMLNPIIYSVKTEIRKGILKFFHKSQA (SEQ ID NO:
263)

ATGCTGGGTCTCAATGGCACCCCCCTTCCAGCCAGCAAACTCCAGCTGACAGGCATTCCCTG
10 GGATACAAACAGGCCTCACCTGGGTTGCCCTGATTTTCTGCATCCTCTACATGATCTCCATT
GTAGGTAACCTCAGCATTCTCACTCTGGTGTTTTGGGAGCCTGCTCTGCATCAGCCCATGT
ACTACTTCCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCTTTTCTACACTTCCCACT
GTGATTTCTACTTTCTGCTTCAACTACAACCATGTTGCGTTTAATGCTTGCTGGTCCAGAT
GTTCTTCATCCACACTTTCTCCTTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC
15 GCTTTGTGGCTATTTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG
GCTATGGGTCTGGGCATCCTTACCAAGAGTTTCACCACTCTCTTCCCTTTCCCTTTTGTGGT
GAAACGACTGCCCTTCTGCAAAGGCAATGTTTTGCATCACTCCTACTGTCTCCATCCAGAT
CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA
TTTTTACCTATGGTATGGACTCAACTTTCATCCTGCTTTCCTACGCATTGATCCTGAGAGCC
20 ATGCTGGTCATCATATCCCAAGGAACAGCGGCTCAAGGCACTCAACACCTGCATGTCACACA
TCTGTGCAGTGTGGCCTTTTATGTGCCATAATTGCTGTCTCCATGATTCACCGCTTCTGG
AAAAGTGCTCCACCTGTTGTTTCATGTCTGATGTCCAATGTCTACCTGTTTGTACCACCCAT
GCTCAACCCTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGATTCTCAAGTTC
TTCCATAAATCCCAGGCCTGA (SEQ ID NO: 264)

25

AOLFR144 sequences:

MGLFNVTHPAFFLLTGIPGLESSHWSLGPLCVMYAVALGGNTVILQAVRVEPSLHEPMMYYFL
SMLSFSDDVAISMATLPTVLRFTCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYVAICD
PLRYATVLTTEVIAAMGLGAAARSFITLPLPFLIKRLPICRSNVLSHSYCLHPDMMRLACADISI
30 NSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS
TVHRFGKHVPCYIHLMSNVYLFVPPVLNPLIYSAKTKEIRRAIFRMFHHIKI (SEQ ID NO: 265)

ATGGGGTTGTTCAATGTCACTCACCTGCATTCTTCCTCCTGACTGGTATCCCTGGTCTGGA
GAGCTCTCACTCCTGGCTGTCAGGGCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA
35 AATACAGTGATCCTGCAGGCTGTGCGAGTGAGGCCAGCCTCCATGAGCCCATGTACTACT
TCCTGTCCATGTTGTCCTTCACTGATGTGGCCATATCCATGGCCACACTGCCCACTGTACTC
CGAACCTTCTGCCTCAATGCCCCGAACATCACTTTTGATGCCTGTCTAATTCAGATGTTTCT
TATTCATTCTTCTCCATGATGGAATCAGGTATTCTGCTGGCCATGAGTTTTGACCGCTATG
TGGCCATTTGTGACCCCTTGCCTATGCAACTGTGCTCACCCTGAAGTCATTGCTGCAAT
40 GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCTTTTCCCTCTTCCCTTTCTTATTAAGA
GGCTGCCTATCTGCAGATCCAATGTTCTTTCTCACTCCTACTGCCTGCACCCAGACATGATG
AGGCTTGCCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTTGTTCTTGTATCCAC
CTTTGGCATGGACCTGTTTTTATCTTCTCTCTCTATGTGCTCATTCTGCGTTCTGTCTATGG
CCACTGCTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTCACATATCCTGGC
45 TGTAATTGCATTTTATGTGCCAATGATTGGGGTCTCCACAGTGCACCGCTTTGGGAAGCAT
GTCCCATGTACATACATGTCTCATGTCAAATGTGTACCTATTTGTGCTCCTGTGCTCAA
CCCTCTCATTTATAGCGCCAAGACAAAGGAAATCCGCCGAGCCATTTTCCGCATGTTTCAC
CACATCAAAATATGA (SEQ ID NO: 266)

AOLFR145 sequences:

MSVQYSLSPQFMILLSNITQFSPIFYLTSPFGLGKHWIFIPFFFMVMVAISGNCFILIIKTNPRLH
 TPMYYLLSLLALDGLGCVSTLPTTMGIFWFNSQSIYFGACQIQMFCHSFSFMESSVLLMMSFD
 RFVAICHPLRYVIIITGQVVRAGLIVIFRGPVATIPVLLLKAFPYCGSVVLSHSFCLHQEVIQLA
 5 CTDTTFNNLYGLMVVFTVMLDLVLIALSYGLILHTVAGLASQEEQRRAFQTCTAHLCAVLVF
 FVPMMLGLSLVHRFGKHAPPAIHLLMANVYLFVPPMLNPIIYSIKTKEIHRAIIKLLGLKKASK
 (SEQ ID NO: 267)

ATGTCAGTCCAATATTCGCTCAGTCCTCAATTTCATGCTGCTATCCAACATTACTCAGTTTAG
 10 CCCCATATTCTATCTCACCAGCTTTCCTGGATTGGAAGGCATCAAACACTGGATTTTCATCC
 CCTTTTTCTTTATGTACATGGTTGCCATCTCAGGCAATTGTTTCATTCTGATCATTATTAAG
 ACCAACCCCTCGTCTGCACACACCCATGTACTATCTACTATCCTTGCTGGCCCTCACTGACCT
 GGGGCTGTGTGTGTCCACGTTGCCACCACTATGGGGATCTTCTGGTTTAACTCCCAGAGT
 ATCTACTTTGGAGCGTGTCAAATCCAGATGTTCTGCATCCACTCTTTTCTTCATGGAGTC
 15 CTCAGTGCTCCTCATGATGTCCTTTGACCGCTTGTGGCCATCTGCCACCCCTCTGAGGTATT
 CGGTCAATTATCACTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTCATCTTCCGGGGACC
 TGTGGCCACTATCCCTATTGTCCTCCTCCTGAAGGCTTTTCCCTACTGTGGATCTGTGGTCC
 TCTCCCACTCATTTTGCCTGCACCAGGAAGTGATACAGCTGGCCTGCACAGATACCACCTT
 CAATAATCTGTATGGACTGATGGTGGTAGTTTCACTGTGATGCTGGACCTGGTGCTCATC
 20 GCATGTCTCTATGGACTCATCTGCACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC
 GCCGTGCCTTTTCAGACATGCACCGCTCATCTCTGTGCTGTGCTAGTATTCTTTGTGCCCATG
 ATGGGGCTGTCCCTGGTGACCGTTTGGGAAGCATGCCCCACCTGCTATTTCATCTTCTTAT
 GGCCAATGTCTACCTTTTTGTGCCTCCCATGCTTAACCAATCATATACAGCATTAAGACC
 AAGGAGATCCACCGTGCCATTATCAAACCTCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ
 25 ID NO: 268)

AOLFR146 sequences:

MSQVTNNTQEGIFYLTDIPGFEASHIWISIPVCCLYTISIMGNNTILTIVIRTEPSVHQRMVFLSM
 LALDGLTLTTLPTVMQLLWFNVRRISSEACFAQFFFLHGFSFMESSVLLAMSVDCYVAICCP
 30 LHYASILTNEVIGRTGLAIICCCVLAVLPSLFLKRLPFCHSHLLSRSYCLHQDMIRLVCADIRLN
 SWYGFALALLHIVDPLLIVISYTLILKNILGTATWAERLRALNNCLSHILAVLVLYIPMVGVSM
 HRFKHA SPLVHVIMANIYLLAPPVMNPIIYSVKNKQIQWGMNLNLSLKNMHSR (SEQ ID NO:
 269)

ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG
 35 GATTTGAGGCCTCCACATCTGGATCTCCATCCCCGTCTGCTGTCTCTACACCATCTCCATC
 ATGGGCAATACCACCATCCTCACTGTCAATCGCACAGAGCCATCTGTCCACCAGCGCATGT
 ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCTCACCACTTACCCACA
 GTCATGCAGCTTCTCTGGTTCAACGTTTCGTAAGTACAGCTCTGAGGCCTGTTTGTCTAGTT
 40 TTTCTTCTTCATGGATTCTCCTTATGGAGTCTTCTGTCTCCTGGCTATGTCGGTTGACT
 GCTATGTGGCCATCTGCTGTCCCCTCCATTATGCCTCCATCCTCACCAATGAAGTCATTGGT
 AGAACTGGGTTAGCCATCATTTGCTGCTGTGTTCTGGCGGTTCTTCCCTCCCTTTTCTTACT
 CAAGCGACTGCCTTTCTGCCACTCCCACCTTCTCTCGCTCCTATTGCCTCCACCAGGATA
 TGATCCGCCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTGCTCTTGCCTT
 45 GCTCATTATTATCGTGGATCCTCTGCTCATTGTGATCTCCTATACACTATTCTGAAAAATA
 TCTTGGGCACAGCCACCTGGGCTGAGCGACTCCGTGCCCTCAATAACTGCCTGTCCACAT
 TCTAGCTGTCTGGTCTCTACATTCCCATGGTTGGTGTATCTATGACTCATCGCTTTGCCA
 AGCATGCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCACCCCGGT
 GATGAACCCCATCATTTACAGTGTAAGAACAAGCAGATCCAATGGGGAATGTTAAATTTT
 50 CTTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

AOLFR147 sequences:

MPSASAMIIIFNLSSYNPGPFILVGIPGLEQFHVWIGIPFCIIYIVAVVGNICLLYLIVVEHSLHEPMF
 FFLSMLAMTDLILSTAGVPKALSIFWLGAAREITFPGLTQMFFLHYNFVLD SAILMAMAFDHYV
 55 AICSPRLRYTTILTPKTHKSAMGISFRSFCILPDVFLTLCLPFCRTRIIPHTYCEHIGVAQLACADISI
 NFWYGFCVPIMTVISDVILIAVSIAHLCAVFLPSQDACQKALGTCGSHVCVILMFYTPAFFSI

LAHRFGHNVSRTFHIMFANLYIVIPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO: 271)

5 ATGCCATCTGCCTCTGCCATGATCATTTTCAACCTGAGCAGTTACAATCCAGGACCCTTCAT
TCTGGTAGGGATCCCAGGCTGGAGCAATTCATGTGTGGATTGGAATTCCTTCTGTATC
ATCTACATTGTAGCTGTTGTGGGAACTGCATCCTTCTCTACCTCATTGTGGTGGAGCATA
GTCTTCATGAACCCATGTTCTTCTTCTCTCCATGCTGGCCATGACTGACCTCATCTTGTCC
ACAGCTGGTGTGCGCTAAAGCACTCAGTATCTTTTGGCTAGGGGCTCGCGAAATCACATTC
10 CAGGATGCCTTACACAAATGTTCTTCTTCACTATAACTTTGTCCTGGATTACGCCATTCTG
ATGGCCATGGCATTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATAACCACCATCTT
GACTCCCAAGACCATCATCAAGAGTGCTATGGGCATCTCCTTTCGAAGCTTCTGCATCATC
CTGCCAGATGTATTCTTGTGCTGACATGCCTGCCTTCTGCAGGACACGCATCATAACCCACA
CATACTGTGAGCATATAGGTGTTGCCAGCTCGCCTGTGCTGATATCTCCATCAACTTCTG
GTATGGCTTTTGTGTTCCCATCATGACGGTCATCTCAGATGTGATTCTCATTGCTGTTTCT
15 ACGCACACATCCTCTGTGCTGTCTTTGGCCTTCCCTCCCAAGATGCCTGCCAGAAAGCCCT
CGGCACTTGTGGTTCTCATGTCTGTGTCATCTCATGTTTATAACCTGCCTTTTTCTCCA
TCCTCGCCATCGCTTGGACACAATGTCTCTCGCACCTTCCACATCATGTTTGCCAATCTC
TACATTGTTATCCACCTGCACTCAACCCCATGGTTACGGAGTGAAGACCAAGCAGATCA
GAGATAAGGTTATACTTTGTTTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

20 **AOLFR148 sequences:**
MPTVNHSGTSHTVFHLLGIPGLQDQHMWISIPFFISYVTALLGNSLLIFILTKRSLHEPMYLFLC
MLAGADIVLSTCTIPQALAFWFRAGDISLDRCTQLFFIHSTFISESGILLVMAFDHYAICYPLR
YTTILTNALIKKICVTVSLRSYGTIFPIFLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINIWYG
25 FSILMSTVVLVDVLFISYMLILHAVFHMPSPDACHKALNTFGSHVCIILFYGSGIFTILTQRFGR
HIPPCIHIPLANVCILAPPMLNPIIYGIKTKQIQEQVVQFLFIKQKITLV (SEQ ID NO: 273)

30 ATGCCTACTGTAAACCACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG
GCCTACAGGACCAGCACATGTGGATTCTATCCATTCTTCATTTCTATGTCACCGCCCTT
CTTGGGAACAGCCTGCTCATCTTCATTATCCTCACAAAGCGCAGCCTCCATGAACCCATGT
ACCTCTTCTCTGCATGCTGGCTGGAGCAGACATTGTCCTCTCCACGTGCACCATTCCTCAG
GCCTTAGCTATCTTCTGGTCCGCTGCTGGGGACATCTCCCTGGATCGTTGCATCACTCAGCT
CTTCTTCATCCATTCCACCTTCATCTCTGAGTCAGGGATCTTGCTGGTGATGGCCTTTGACC
ACTATATTGCCATATGCTACCCACTGAGGTACACCACCATCTTACAAATGCTCTGATCAA
35 GAAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTTCCCTATCATATTTCTT
TAAAAAGATTGACTTTCTGCCAGAATAATATTATCCACACACCTTTTGTGAACACATTGG
CCTAGCCAAATATGCATGTAATGACATTCGAATAAACATTTGGTATGGGTTTTCCATTCTA
ATGTCGACGGTGGTCTTAGATGTTGTACTAATTTTATTTCCTATATGCTGATTCTCCATGC
TGTCTTCCACATGCCTTCTCCAGATGCTTGCCACAAAGCTCTCAACACATTTGGCTCCCATG
40 TCTGCATCATCATCTCTTTTATGGGTCTGGCATCTTCACAATCCTTACCCAGAGGTTTGA
CGCCACATTCCACCTTGTATCCACATCCCGTTGGCTAATGTCTGCATTCTGGCTCCACCTAT
GCTGAATCCCATTATTTATGGGATCAAAACCAAGCAAATCCAGGAACAGGTGGTTCAGTTT
TTGTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)

45 **AOLFR149 sequences:**
MSNASLLTAFILMGLPHAPALDAPLFGVFLVVYVLTVLGNLLILLVIRVDSHLHTTMYFYLTNL
SFIDMWFSTVTVPKLLMTLVFPSGRAISFHSMAQLYFFHFLGGTECFLYRVMSCDRYLAYSYP
LRYTSMMTGRSCTLLATSTWLSGSLHSAVQAILTFHLPYCGPNWQHYLCDAPPILKLACADTS
AIETVIFVTGIVASGCFVLIVLSYVSIVCSILRIRTSEGHRAFTQCASHCIVVLCCFFGPGLFIYLR
50 PGSRKAVDGVVAVFYTVLTPLLNPVYTLRNKEVKKALLKLKDKVAHSQSK (SEQ ID NO: 275)

55 ATGTCCAACGCCAGCCTACTGACAGCGTTCATCCTCATGGGCCTTCCCCATGCCCCAGCGC
TGGACGCCCCCTCTTGGAGTCTTCTGGTGGTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTACTACTTCTCTA
CCAACCTGTCGTTCAATTGACATGTGGTCTCCACTGTCACGGTGCCCAAATTGCTGATGAC

TTTGGTGTTCCTCAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCTATTTCT
TTCACCTCCTAGGGGGACCGAGTGTTCCTCTACAGGGTCATGCTCTGTGATCGCTACCT
GGCCATCAGTTACCCGCTCAGGTACACCAGCATGATGACTGGGCGCTCGTGTACTCTTCTG
GCCACCAGCACTTGGCTCAGTGGCTCTCTGCACCTGCTGTCCAGGCCATATTGACTTTCC
5 ATTTGCCCTACTGTGGACCCAACTGGATCCAGCACTATTTGTGTGATGCACCGCCCATCT
GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCATTTTTGTGACTGTTGGAATA
GTGGCCTCGGGCTGCTTTGTCTGATAGTGTCTATGTGTCCATCGTCTGTTCCATCCT
GCGGATCCGCACCTCAGAGGGGAAGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCATTTACCTGAGGCCAGGCTCCAGGAAAGC
10 TGTGGATGGAGTTGTGGCCGTTTTCTACACTGTGCTGACGCCCCCTTCTCAACCCTGTTGTGT
ACACCCTGAGGAACAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCAC
ATTCTCAGAGCAAATAG (SEQ ID NO: 276)

AOLFR150 sequences:

15 MELGNVTRVKEFIFLGLTQSQDQSLVFLFLCLVYMTTLLGNLLIMVTVTCESSLHTPMYFLLR
NLAILDICFSSTAPKVLDDLLSKKKTISYTSMTQIFLHLLGGADIFLSVMAFDCYMAISKPL
HYVTIMSRGQCTALISASWMGGFVHSIVQISLLPLPFCGPNVLDTFYCDVPQVLKLTCTDTFA
LEFLMISNNGLVTTLWFIFLLVSYTVILMTLRSQAGGGRRKAISTCTSPHHCGBPFCALHLCLC
PALHCPPHRKGHLCHLHCHLPSAEPDLHSEEPGNEVSHEKTEKTRAF (SEQ ID NO: 277)

20 ATGGAGTTGGGAAATGTCACCAGAGTAAAAGAATTTATATTTCTGGGACTTACTCAATCCC
AAGACCAGAGTTTGGTCTTGTTCCTTTTTTATGTCTTGTGTACATGACGACTCTGCTGGGA
AACCTCCTCATCATGGTCACCGTGACCTGTGAGTCTCGCCTTCACACCCCATGTACTTCCT
GCTCCGCAATCTAGCCATCCTTGACATCTGCTTCTCCTCCACAACTGCTCCTAAAGTCTTGC
25 TGGACCTTCTGTCAAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTTCT
CTTCCACCTCCTTGGTGGGGCAGACATTTTTTCTCTCTCTGTGATGGCGTTTGACTGCTACA
TGGCCATCTCCAAGCCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT
CATCTCTGCCTCTTGGATGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTTGCTGC
CTCTCCCTTTCTGTGGACCCAATGTTCTTGACACTTCTACTGCGATGTCCCCAGGTCCTC
30 AAACCTCACTTGCACTGACACTTTTGCTCTTGAGTCTTGATGATTTCCAACAATGGCCTGGT
CACTACCCTGTGGTTTATCTTCTGCTTGTGTCTACACAGTCATCCTAATGACGCTGAGGT
CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTGCACCTCCCCACATCACTGTG
GTGACCTGCATTTTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCAC
AGAAAAGGCCATCTCTGTACCTTCACCTGCTATCTCCCTCTGCTGAACCCCTTGATCTACA
35 CTCTGAGGAACCAGGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT
CTGA (SEQ ID NO: 278)

AOLFR151 sequences:

40 MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLIRTNSHLQTPMYFFLGHL
FVDICYSSNVTNMLHNFLEQKTISYAGCFTQCLLFIALVITEFYILASMAIDRYVAICSPLHYS
SRMSKNICVCLVTIPYMYGFLSGFSQSLLTFHLSFCGSLEINHFCADPPLIMLACSDTRVKKMA
MFVVAGFNLSSSLFIILLSYLFIFAAIFRIRSAEGRHKAFSTCASHLTIVTLFYGTLFCMYVRPSE
KSVEESKITAVFYTLSPMLNPLIYSLRNTDILAMQQMIRGKSFHKIAV (SEQ ID NO: 279)

45 ATGTTCTCCCCAAACCACACCATAGTGACAGAATTCATTCTCTTGGGACTGACAGACGACC
CAGTGCTAGAGAAGATCCTGTTTGGGGTATTCTTGCATCTACCTAATCACACTGGCAGG
CAACCTGTGCATGATCCTGCTGATCAGGACCAATTCCCACCTGCAAACACCCATGTATTTCT
TTCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTTACTCCAAATATGCT
GCACAATTTCTCTCAGAACAGAAAGACCATCTCCTACGCTGGATGCTTCACACAGTGTCTT
50 CTCTTCATCGCCCTGGTGATCACTGAGTTTACATCCTTGCTTCAATGGCATTGGATCGCTA
TGTAGCCATTTGCAGCCCTTTGCATTACAGTTCCAGGATGTCCAAGAACATCTGTGTCTGT
CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTTCTCTCAGTCACTGCTAACCTT
TCACTATCCTTCTGTGGCTCCCTTGAAATCAATCATTTCTACTGCGCTGATCCTCCTCTTA
TCATGCTGGCCTGCTCTGACACCCGTGTCAAAAAGATGGCAATGTTTGTAGTTGCAGGCTT
55 TAATCTCTCAAGCTCTCTCTTCATCATTCTCTGTCTATCTTTTCATTTTGCAGCGATCTT
CAGGATCCGTTCTGCTGAAGGCAGGCACAAAGCCTTTTCTACGTGTGCTTCCCACTGACA

AOLFR156 sequences:

MCWAMPSPFTGSSTRNMESRNQSTVTEFIFTGFPQLQDGSLLYFFPLLFYTFIHDNLLIFSAVRL
DTHLGNPMYNFISIFSLEIWTATIPKMLSNLISEKKAISMTGCILQMYFFHSLNSEGILLTT
MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGLILLPEIVMISTLPFCGPNQIHQIFCDLVP
5 VLSLACTDTSMLIEDVIHAVTHIITFLIHALSYVRIVTVILRIPSSEGRQKAXSTCAGHLMVFLIFFG
SVSLMYLRFSNTYPPVLDTAIALMFTVLAPFFNPIIYSLRNKDMNNAIKKLFCLQKVLNKPGG
(SEQ ID NO: 285)

ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA
10 ACCAATCAACAGTGACTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT
CCTGTACTTCTTTCTTTACTTTTCATCTATACTTTTATTATCATTGATAACTTATTAATCTT
CTCTGCTGTAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT
CCTTCTGGAGATCTGGTACACCACAGCCACCATTCCCAAGATGCTCTCCAACCTCATCAG
TGAAAAGAAGGCCATCTCAATGACTGGCTGCATCTTGACAGATGTATTCTTCCACTCACTT
15 GAAAACTCAGAGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA
ACCCTCTTCGCTATCAAATGATCATGACCCCCCGGCTCTGTGCTCACCTCTCTGCAGGTTCC
TGCCTCTTCGGTTTCCTTATCCTGCTTCCCGAGATTGTGATGATTTCCACACTGCCTTTCTG
TGGGCCCAACCAAATCCATCAGATCTTCTGTGACTTGGTCCCTGTGCTAAGCCTGGCCTGT
ACAGACACGTCCATGATTCTGATTGAGGATGTGATTCATGCTGTGACCATCATCATTACCT
20 TCCTAATCATTGCCCTGTCTATGTAAGAATTGTCACTGTGATATTGAGGATTCCTTCTTCT
GAAGGGAGGCAAAAGGCTNTTCTACCTGTGCAGGCCACCTCATGGTCTTCTGATATTCT
TTGGCAGTGTATCACTCATGTACTTGCCTTTCAGCAACACTTATCCACCAGTTTGGACAC
AGCCATTGCACTGATGTTTACTGTACTTGTCTCCATTCTTCAATCCCATCATTTATAGCCTGA
GAAACAAGGACATGAACAATGCAATTAATAAACTGTTCTGTCTCAAAAAGTGTGAACA
25 AGCCTGGAGGTAA (SEQ ID NO: 286)

AOLFR157 sequences:

MAMDNVTAVFQFLIGISNYPQWRDTFFTLVLIHYLSTLLGNGFMIFLIHFDPNLHTPIYFFLSNL
30 SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAISNP
LRYSVVMNGPVCVCLVATSWGTSLVLTAMLILSLRLHFCGANVINHFACEILSLIKLTCSDTSL
NEFMILITSIFTLLLPGFVLLSYIRIAMAIIRISLQGRLLKFTTCGSHLTVVTIFYGSAISMYMKT
QSKSSPDQDKFISVFYGALTPMLNPLIYSLRKKDVKRAIRKVMLKRT (SEQ ID NO: 287)

ATGGCCATGGACAATGTACAGCAGTGTTTCACTTCTCTTATTGGCATTCTAACTATCC
35 TCAATGGAGAGACACGTTTTTACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG
AATGGATTTATGATCTTTCTTATTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT
CCTTAGTAACCTGTCTTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG
TGCATTGTTTCTTACCCATCCCTACCTCTCTTATCCCCGATGTTTGGCTCAAACGAGTGTC
40 TCCTTGGCTTTGGCCACAGCAGAGTGCTCCTACTGGCTGCCATGGCCTATGACCGTGTGG
TTGCTATCAGCAATCCCCTGCGTTATTCACTGGTTATGAATGGCCCAGTGTGTGTCTGCTT
GGTTGCTACCTCATGGGGGACATCACTTGTGCTCACTGCCATGCTCATCCTATCCCTGAGG
CTTCACTTCTGTGGGGGTAATGTCAATCAACATTTTGCTGTGAGATTCTCTCCCTCATTA
GCTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCATCACCAGTATCTTACCC
45 TGCTGCTACCATTTGGGTTTGTCTCTCTCTACATACGAATTGCTATGGCTATCATAAGG
ATTCGCTCACTCCAGGGCAGGCTCAAGGCCTTACCACATGTGGCTCTCACCTGACCGTGG
TGACAATCTTCTATGGGTCAGCCATCTCCATGTATATGAAAACCTCAGTCCAAGTCCTCCCC
TGACCAGGACAAGTTTATCTCAGTGTTTTATGGAGCTTTGACACCCATGTTGAACCCCTG
ATATATAGCCTGAGAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAAGG
50 ACATGA (SEQ ID NO: 288)

AOLFR158 sequences:

MKAGNFSDTPEFFLLGLSGDPELQPIFLFSLMYLATMLGNLLIILAVNSDSLHTPMYFLLSI
LSLVDICFTSTTMPKMLVNIQAQAQSYNTGCLTQICFVLVFGLENGILVMMAYDRFVAICHP
55 LRYNVIMNPKLCGLLLLLSFIVSVLDALLHTLMVLQTLFCIDLEIPHFCELAHILKLACSDVLIN
NILVYLVTSLLGVVPLSGIIFSYTRIVSSVMKIPSAAGGKYKAFSICGSHLIVVSLFYGTGFGVYLS
GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKDMMLKALRKLISRIPSFH (SEQ ID NO: 289)

ATGAAAGCAGGAAACTTCTCAGACACTCCAGAATTCTTTCTCTTGGGATTGTCAGGGGATC
CGGAGCTGCAGCCCATCCTCTTCATGCTGTTCCCTGTCCATGTACCTGGCCACAATGCTGGG
5 GAACCTGCTCATCATCCTGGCCGTCAACTCTGACTCCCACCTCCACACCCCCATGTACTTCC
TCCTCTCTATCCTGTCCTTGGTCGACATCTGTTTACCTCCACCACGATGCCAAAGATGCTG
GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTCACCCAAATCTGCT
TTGTCCTGGTTTTTGTGATTGGAAAATGGAATTCTGGTCATGATGGCCTATGATCGATT
TGTGGCCATCTGTCACCCACTGAGGTACAATGTCATCATGAACCCCAAACTCTGTGGGCTG
10 CTGCTTCTGCTGTCCTTCATCGTTAGTGTCTGCTGGATGCTCTGCTGCACACGTTGATGGTGTCT
ACAGCTGACCTTCTGCATAGACCTGGAAATTCCCCACTTTTTCTGTGAACTAGCTCATATTC
TCAAGCTCGCCTGTTCTGATGTCTCTCATCAATAACATCCTGGTGTATTTGGTGACCAGCCT
GTTAGGTGTTGTTCTCTCTGCGATCATTTTCTCTTACACACGAATTGTCTCCTCTGTCA
TGAAAATTCCATCAGCTGGTGGAAAGTATAAAGCTTTTCCATCTGCGGGTCACATTAAAT
CGTTGTTTCTTGTGTTTATGGAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGCTACCCACT
15 CCTCCAGGAAGGGTGAATAGCATCAGTGATGTATACCGTGGTCACCCCATGCTGAACCC
ACTCATTTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAACTAATATCTAG
GATACCATCTTTCCATTGA (SEQ ID NO: 290)

AOLFR159 sequences:

20 MGPRNQTA VSEFLLMKVTEDPELKLIPFSLFLSMYLVTLGNLLILLAVISDSHLHTPMYFLLFN
LSFTDICLTTTTVPKILVNIQAQNSITYTGCLTQICLVLFAGLESCFLAVMAYDRYVAICHPL
RYTVLMNVHFWGLLILLSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCEVVQVIKLACSDTL
INNILIYFASSVFGAIPLSGIIFSYSQIVTSVLRMP SARGKYKAFSTCGCHLSVFSFYGTAFGVYIS
SAVAESSRITAVASVMYTVVPQMMNPFYSLRNKEMKKALRKLIGRLFPF (SEQ ID NO: 291)

25 ATGGGACCCAGAAACCAAACAGCTGTTTCAGAATTTCTTCTCATGAAAGTGACAGAGGAC
CCAGAACTGAAGTTAATCCCTTTCAGCCTGTTCTGTCCATGTACCTGGTCACCATCCTGG
GGAACCTGCTCATTCTCCTGGCTGTCATCTCTGACTCCCACCTCCACACCCCCATGTACTTC
CTTCTCTTTAATCTCTCCTTTACTGACATCTGTTTAAACCACAACCACAGTCCCAAAGATCCT
30 AGTGAACATCCAAGCTCAGAATCAGAGTATCACTTACACAGGCTGCCTCACCCAGATCTGT
CTTGCTTTGGTTTTTGTGCTGGCTTGGAAAGTTGCTTTCTTGCAGTCATGGCCTACGACCGCTA
TGTGGCCATTGCCACCCACTGAGGTACACAGTCCTCATGAATGTCCATTTCTGGGGCTTG
CTGATTCTTCTCTCCATGTTTCATGAGCACTATGGATGCCCTGGTTCAGAGTCTGATGGTATT
GCAGCTGTCCTTCTGCAAAAACGTTGAAATCCCTTTGTTCTTCTGTGAAGTCGTTACAGTCT
35 ATCAAGCTCGCCTGTTCTGACACCCTCATCAACAACATCCTCATATATTTGCAAGTAGTGT
ATTTGGTGCAATTCCTCTCTCTGGAATAATTTTCTCTTATTCTCAAATAGTCACCTCTGTTT
TGAGAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTTCCACCTGTGGCTGTCACCTCTC
TGTTTTTCTCTTGTCTATGGGACAGCTTTTGGGGTGTACATTAGTTCTGCTGTTGCTGAGT
CTTCCCGAATTACTGCTGTGGCTTCACTGTGATGTACACTGTGGTCCCTCAAATGATGAACCC
40 CTTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAACTTATTGGTAG
GCTGTTTCCTTTTAG (SEQ ID NO: 292)

AOLFR160 sequences:

45 MPMQLLLTDFIIFSIRFIINSMEARNQTAISKFLLGLIEDPELQPVLFSLFLSMYLVTLGNLLILL
AVISDSHLHTPMYFFLSNLSFLDICLSTTTPKMLVNIQAQNSITYSGCLTQICFVLFAGLENC
LLAAMAYDRYVAICHPLRYTVIMNPRLCGLLILLSLLTSVNNALLLSLMVLRSLFCTDLEIPLFF
CELAQVIQLTCSDTLINNILIYFAACIFGGVPLSGIILSYTQITSCVLRMP SASGKHKA VSTCGSHL
SIVLLFYGAGLGVISSVVTDSPRKTAVASVMYSVFPQMVNPFYSLRNKDMKGLRKFGRIP
SLLWCAICFGFRFLE (SEQ ID NO: 293)

50 ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTTCCATCAGATTCATCATCAACAG
CATGGAAGCGAGAAACCAAACAGCTATTTCAAAATTCCTTCTCCTGGGACTGATAGAGGAT
CCGGAATGCAGCCCGTCTCTTTCAGCCTGTCTCTGTCCATGTACTTGGTCACCATCCTGGG
GAACCTGCTCATCCTCTTGGCTGTCATCTGACTCTCACCTCCACACCCCCATGTACTTCT
55 TCCTCTCCAATCTCTCCTTTTGGACATTTGTTTAAAGCACAAACCACGATCCCAAAGATGCTG
GTGAACATCCAAGCTCAGAATCGGAGCATCACGTACTCAGGCTGCCTCACCCAGATCTGCT

TTGTCTTGTTTTTGGCTGGCTTGGAAAATTGTCTCCTTGCAGCAATGGCCTATGACCGCTAT
 GTGGCCATTTGTCACCCCCTTAGATACACAGTCATCATGAACCCCCGCTCTGTGGCCTGC
 TGATTCTTCTCTCTCTGTTGACTAGTGTGTGAATGCCCTTCTTCTCAGCCTGATGGTGTG
 5 AGGCTGTCTTCTGACAGACCTGGAATCCCGCTCTTCTTCTGTGAAGTGGCTCAGGTCA
 TCCAACCTCACCTGTTTACAGACACCTCATCAATAACATCCTGATATATTTTGCAGCTTGATA
 TTTGGTGGTGTTCCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACCTCCTGTGTTTT
 GAGAATGCCATCAGCAAGTGGAAAGCACAAAGCAGTTTCCACCTGTGGGTCTCACCTCTCC
 ATTGTTCTCTTGTCTATGGGGCAGGTTTGGGGGTGTACATTAGTTCTGTGGTTACTGACTC
 10 ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTGTTCCCTCAAATGGTGAACCCC
 TTTATCTATAGTCTGAGGAATAAGGACATGAAGGAACCTTGAGGAAGTTCATAGGGAGG
 ATACCTTCTCTTCTGTGGTGTGCCATTTGCTTTGGATTACAGGTTTCTAGAGTAA (SEQ ID
 NO: 294)

AOLFR161 sequences:

15 MEPRNQTSASQFILLGLSEKPEQETLLFSLFFCMYLMVMVGNLLHLAISIDSHLHTPMYFFLANL
 SLVDFCLATNTIPKMLVSLQTGSKAISYPCCLIQMYFFHFFGIVDSVIIAMMAYDRFVAICHPLH
 YAKIMSLRLCRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR
 IFILIVAGMVIATPFVCILASYARILVAIMKVPASAGGRKKAFTSCSSHLVVALFYGTITGVYLCF
 20 SSVLTTVKEKASAVMYTAVTPMLNPFYISLRNRDLKGALRKLVRKITSSS (SEQ ID NO: 295)

ATGGAACCAAGAAACCAAACCAAGTGCATCTCAATTCATCCTCCTGGGACTCTCAGAAAAGC
 CAGAGCAGGAGACGCTTCTCTTTTCCCTGTTCTTCTGCATGTACCTGGTCATGGTCGTGGG
 GAACCTGCTCATCATCCTGGCCATCAGCATAGACTCCCACCTCCACACCCCCATGTACTTCT
 25 TCCTGGCCAACCTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCCTAAGATGCT
 GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCCTGATCCAGATGTAC
 TTCTTCCATTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGTT
 CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTGCGCTG
 CTGGTCGGCGCCCTCTGGGCGTTTTCTGCTTCATCTCACTCACTCACATCCTCCTGATGGC
 CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC
 30 TCCGACTTTCGTGCACGGACACCTCTGTGAATAGGATCTTCATCCTCATTGTGGCAGGGAT
 GGTGATAGCCACGCCCTTTGTCTGCATCCTGGCCTCCTATGCTCGCATCCTTGTGGCCATCA
 TGAAGGTCCCCTCTGCAGGCGGCAGGAAGAAAGCCTTCTCCACCTGCAGCTCCCACCTGTC
 TGTGGTTGCTCTCTTCTATGGGACCACCATTTGGCGTCTATCTGTGTCCCTCCTCGGTCTCA
 CCACTGTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCAACCCCATGCTGAATCC
 35 CTTATCTACAGCTTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG
 AAAGATCACCTCATCTTCTGA (SEQ ID NO: 296)

AOLFR162 sequences:

40 MMRLMKEVRGRNQTEVTEFLLLGLSDNPDQGVLFALFLLIYMANMVGNLGMIVLIKIDLCCLH
 TPMYFFLSSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFFGSFLGTECFLLAMMA
 YDRYAAIWNPLLYPVLVSGRICFLLIATSFLAGCGNAIHTGMTFRLSFCGSNRINHFYCDTPPL
 LKLSGSDTHFNGIVIMAFSSFIVISCVMIVLISYLCIFIAVLKMPISLEGRHKAFSTCASYLMAVTIF
 FGILFMYLRPTSSYSMEQDKVVSFYTVIIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID
 NO: 297)

45 ATGATGAGACTTATGAAAGAGGTTTCGAGGCAGAAATCAAACAGAAGTAACAGAATTTCTC
 CTCTTAGGACTTTCCGACAATCCAGATCTACAAGGAGTCCTCTTTGCATTGTTTCTGTTGAT
 CTATATGGCAAACATGGTGGGCAATTTGGGGATGATTGTATTGATTAAGATTGATCTCTGT
 50 CTCCACACCCCCATGTATTTCTTCTCAGTAGCCTCTCTTTTGTAGATGCCTCTTACTCTTCT
 TCCGTCACTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCATG
 GATGTGCTGCCAGTTCTACTTCTTTGGCTCCTTCTCTGGGACTGAGTGCTTCTGTTGGCC
 ATGATGGCATATGACCGCTATGCAGCTTTGGAACCCCTGCTCTACCCAGTTCTCGTGT
 CTGGGAGAATTTGCTTTTTGCTAATAGCTACCTCCTTCTTAGCAGGTTGTGGAATGCAGC
 CATAACATACAGGGATGACTTTTAGGTTGTCCTTTTGTGGTTCTAATAGGATCAACCATTTCT
 55 ACTGTGACACCCCGCCACTGCTCAAACCTCTTGTCTGATACCCACTTCAATGGCATTGTG
 ATCATGGCATTCTCAAGTTTATTGTGCATCAGCTGTGTTATGATTGTCCTCATTTCTACCT

5 GTGTATCTTCATTGCCGTCTTGAAGATGCCTTCGTTAGAGGGCAGGCACAAAGCCTTCTCC
ACCTGTGCCTCTTACCTCATGGCTGTCACCATATTCTTTGGAACAATCCTCTTCATGTACTT
GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTTGTCTCTGTCTTTTATACAGTA
ATAATCCCTGTGCTAAATCCCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCC
TAAAGAAGATCTTATGGAAACACATCTTGTAG (SEQ ID NO: 298)

AOLFR163 sequences:

10 MQRSNHTVTEFILLGFTTDPGMQLGLFVVFLGVYSLTVVGNSTLIVLICNDSCLHTPMYFFTGN
LSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL
LYAQAMSIKLCALLVAVSYCGGFINSIIKKTFSNFCRENIIDDFCDLLPLVELACGEKGGYK
IMMYFLLASNVICPAVLILASYLFIITSVLRISSSKGYLKAFTSCSSHLTSVTLYYGSILYIYALPRS
SYSFDMKIVSTFYTVVFPMLNLMYSLRNKDVKEALKKLLP (SEQ ID NO: 299)

15 ATGCAGAGGAGCAATCATACAGTGACTGAGTTTATACTGCTGGGCTTCACCACAGACCCA
GGAATGCAGCTGGGCCTCTTCGTGGTGTCTCTGGGCGTGTACTCTCTCACTGTGGTAGGAA
ATAGCACCCTCATCGTGTGATCTGTAATGACTCCTGCCTCCACACACCCATGTATTTTTTC
ACTGGAAATCTGTCGTTTCTGGATCTCTGGTATTCTTCTGTCTACACCCCAAAGATCCTAGT
GACCTGCATCTCTGAAGACAAAAGCATCTCCTTGTCTGGCTGCCTGTGTCAAGTCTCTTCTTCT
CTGCAGGGCTGGCCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT
20 GGCCATCTCCAAGCCCCTGCTTTATGCCAGGCCATGTCCATAAAGCTGTGTGCATTGCTG
GTAGCAGTCTCATATTGTGGTGGCTTTATTAACCTCTTCAATCATCACCAGAAAACGTTTTTC
CTTTAACTTCTGCCGTGAAAACATCATTGATGACTTTTTCTGTGATTTGCTTCCCTTGGTGG
AGCTGGCCTGTGGCGAGAAGGGCGGCTATAAAATTATGATGTACTTCTGCTGGCCTCCAA
TGTCATCTGCCCGCAGTGTCTCATCTGGCCTCCTACCTCTTTATCATCACCAGTGTCTTGA
25 GGATCTCCTCCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCCTCCCACCTGACCTCT
GTCACCTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCCAGATCTAGTATTCTTT
TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATTCCCCATGTTGAATCTCATG
ATCTACAGCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAAGTCTCTCCATAA (SEQ
ID NO: 300)

30

AOLFR164 sequences:

35 MFLTERNTTSEATFTLLGFS DYLELQIPLFFVFLAVYGFSVVGNLGMIVIIKINPKLHTPMYFFLN
HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFCTFVVTELILFAVMA YDHFVAICNP
LLYTVAISQKLCAMLVVVLYAWGVACSLTLACSALKLSFHGFNTINHFFCELSSLISLSPDYSYL
SQLLLFTVATFNEISTLLIILTSYAFIIVTTLKMPASGHRKVFSTCASHLTAITIFHGTLFLYCVP
NSKNSRHTVKVASVFYTVVIPLLNPLIYSLRNKDVKDAIRKIINTKYFHIKHRHWYPN FVIEQ
(SEQ ID NO: 301)

40 ATGTTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACCTCTCTTGGGCTTCTCAG
ATTACCTGGAAGTCAAATTCCTCTCTTTGTATTTCTGGCAGTCTACGGCTTCAGTGTG
GTAGGGAATCTTGGGATGATAGTGATCATCAAATTAACCCAAAATTGCATACCCCATGT
ATTTTTCTCTCAACCACCTCTCCTTTGTGGATTTCTGCTATTCTCCTCCATCATTGCTCCCATGA
TGCTGGTGAACCTGGTTGTAGAAGATAGAACCATTTCATTCTCAGGATGTTTGGTGCAATT
45 CTTTTCTTTTGACCTTTGTAGTGACTGAATTAATTCTATTGCGGTGATGGCCTATGACC
ACTTTGTGGCCATTTGCAATCCTCTGCTCTACACAGTTGCCATCTCCCAGAAACTCTGTGCC
ATGCTGGTGGTTGTATTGTATGCATGGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG
CTTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTTCTTCTGTGAGTTATCCTCC
CTGATATCACTCTCTTACCCTGACTCTTATCTCAGCCAGTTGCTTCTTTTCACTGTTGCCAC
TTTAAAGAGATAAGCACACTACTCATCTTCTGACATCTTATGCATTTCATCATTGTCCACCA
50 CCTGAAGATGCCTTCAGCCAGTGGGACCCGCAAGTCTTCTCCACCTGTGCCTCCCACCT
GACTGCCATCACCATCTTCCATGGCACCCTCTTCTCCTCTACTGTGTACCCAACTCCAAAA
ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTACACCGTGGTGATCCCCTTGTGAA
TCCCCTGATCTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT
ACAAAATATTTTCATATTAAACATAGGCATTGGTATCCATTTAATTTTGTATTGAACAATA
55 A (SEQ ID NO: 302)

AOLFR165 sequences:

MAVGRNNTIVTKFILLGLSDHPQMKIFLFMLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL
 SNLSFLDICYVSSTAPKMLSIIITEQKTISFVGCATQYFVFCGMGLTECFLLAAMAYDRYAAICN
 PLYTIVLISHTLCLKMVVGAYVGGFLSSFIETYSVYQHDFCGPYMINHFFCDLPPVLALSCSDTF
 5 TSEVVTFIVSVVVGIVSVLVVLISYGYIVAADVVKISSATGRTKAFSTCASHLTAVTLFYGSGFFM
 YMRPSSSYSLNRDKVVSIFYALVIPVNPPIYSFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG
 (SEQ ID NO: 303)

ATGGCTGTAGGAAGGAACAACAATTGTGACAAAATTCATTCTCCTGGGACTTTCAGACC
 10 ATCCTCAAATGAAGATTTTCCTTTTCATGTTATTTCTGGGGCTCTACCTCCTGACGTTGGCC
 TGGAACCTAAGCCTCATTGCCCTCATTAAAGATGGACTCTCACCTGCACATGCCCATGTACT
 TCTTCCTCAGTAACCTGTCTTCCTGGACATCTGCTATGTGTCTCCACCGCCCCAAGATG
 CTGTCTGACATCATCACAGAGCAGAAAACCATTTCTTTGTTGGCTGTGCCACTCAGTACT
 TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTTCTCCTGGCAGCTATGGCCTATGACCG
 15 GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCCTCATATCCCATAACACTTTGTTTAA
 AGATGGTGGTTGGCGCCTATGTGGGTGGATTCTTAGTTCTTTTCATTGAAACATACTCTGT
 CTATCAGCATGATTTCTGTGGGCCCTATATGATCAACCACTTTTTCTGTGACCTCCCTCCAG
 TCTGGCTCTGTCTGCTCTGATACCTTACCAGCGAGGTGGTGACCTTCATAGTCAGTGTT
 20 GTCGTTGGAATAGTGTCTGTGCTAGTGGTCCTCATCTCTTATGGTTACATTGTTGCTGCTGT
 TGTGAAGATCAGCTCAGCTACAGGTAGGACAAGGCCTTCAGCACTTGTGCTCTCACCTG
 ACTGCTGTGACCTCTTCTATGGTTCTGGATTCTTCATGTACATGCGACCCAGTCCAGCTA
 CTCCCTAAACAGGGACAAGGTGGTGCCATATTCTATGCCTTGGTGATCCCCGTGGTGAAT
 CCCATCATCTACAGTTTTAGGAATAAGGAGATTAAAAATGCCATGAGGAAAGCCATGGAA
 AGGGACCCCGGGATTTCTCACGGTGGACCATTCATTTTATGACCTTGGGCTAA (SEQ ID
 25 NO: 304)

AOLFR166 sequences:

MEMENCTRVKEFIFLGLTQNREVSIVLFLFLLLVYVTTLLGNLLIMVTVTCESRLHTPMYFLLH
 NLSIADICFSSITVPKVLVDLLSERKTISFNHCFTQMFLFHLIGVDVFSLSVMALDRYVAISKPL
 30 HYATIMSRDHCIGLTVAAWLGGFVHSIVQISLLPLPFCGPNVLDTFYCDVHRVLKLAHTDIFIL
 ELLMISNNGLLTTLWFFLLVSYIVILSLPKSQAGEGRRKAISTCTSHITVTVTLHFVPCIYVYARP
 FTALPMDKAISVTFVISPLLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

ATGGAGATGGAAAACCTGCACCAGGGTAAAAGAATTTATTTTCCTTGGCCTGACCCAGAATC
 35 GGGAAGTGAGCTTAGTCTTATTTCTTTTCCTACTCTTGGTGTATGTGACAACTTGTGGGA
 AACCTCCTCATCATGGTCACTGTTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTTT
 GCTCCATAATTTATCTATTGCCGATATCTGCTTCTCTCCATCACAGTGCCCAAGGTTCTGG
 TGGACCTTCTGTCTGAAAGAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA
 TTCCACCTTATTGGAGGGGTGGATGATTTTCTCTTTCGGTGATGGCATTGGATCGATATG
 40 TGGCCATCTCCAAGCCCCTGCACTATGCGACTATCATGAGTAGAGACCATTGCATTGGGCT
 CACAGTGGCTGCCTGGTTGGGGGGCTTTGTCCACTCCATCGTGACAGATTTCCCTGTTGCTC
 CCACTCCCTTTCTGCGGACCCAATGTTCTTGACACTTTCTACTGTGATGTCCACCGGGTCT
 CAAACTGGCCCATACAGACATTTTCATACTTGAACCTACTAATGATTCCAACAATGGACTG
 CTCACCACACTGTGGTTTTCTGCTGCTGCTGCTACATAGTCATATTATCATTACCCAA
 45 GTCTCAGGCAGGAGAGGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCCACATCACTGT
 GGTGACCTGCATTTCTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCA
 TGGATAAGGCCATCTCTGTACCTTCACTGTCTATCTCCCTCTGCTCAACCCCTTGATCTAC
 ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCCT
 TCTGATAGAAAATAG *SEQ ID NO: 306)

AOLFR167 sequences:

MSITKAWNSSSVTMFILLGFTDHPQLALLFVTFGLGIYLLTLAWNLAFLIRGDTHLHTPMYFF
 LSNLSFDICYSSAVAPNMLTDFWEQKTISFVGCAAQFFFFVGMGLSECLLLTAMAYDRYAAI
 55 SSPLLYPTIMTQGLCTRMVVGAYVGGFLSSLIQASSIFRLHFCGPNINHFFCDLPPVLALSCSDT
 FLSQVVNFLVVVTVGGTSFLQLLISYGYIVSAVLKIPSAEGRWKACNTCASHLMVVTLFLGTAL

FVYLRPSSSYLLGRDKVVSFVYSLVIPMLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID NO: 307)

5 ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCCTCCTGGGATTCA
CAGACCATCCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCCTGGGCATCTATCTTACCACC
CTGGCCTGGAACCTGGCCCTCATTTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA
TGTACTTCTTCTTAAGCAACTTATCTTTTCATTGACATCTGCTACTCTTCTGCTGTGGCTCCC
AATATGCTCACTGACTTCTTCTGGGAGCAGAAGACCATATCATTTGTGGGCTGTGCTGCTC
AGTTTTTTTTCTTTGTGCGCATGGGTCTGTCTGAGTGCCTCCTCCTGACTGCTATGGCATAAC
10 GACCGATATGCAGCCATCTCCAGCCCCCTTCTCTACCCCACTATCATGACCCAGGGCCTCT
GTACACGCATGGTGGTTGGGGCATATGTTGGTGGCTTCCTGAGCTCCCTGATCCAGGCCAG
CTCCATATTTAGGCTTCACTTTTGC GGACCCAACATCATCAACCACTTCTTCTGCGACCTCC
CACCAGTCTGCTGTCTGTCTGCTCTGACACCTTCCTCAGTCAAGTGGTGAATTTCTCCTCGTG
GTGGTCACTGTGCGAGGAACATCGTTCTCCTCAACTCCTTATCTCCTATGGTTACATAGTGT
15 CTGCGGTCTGAAGATCCCTCAGCAGAGGGCCGATGGAAAGCCTGCAACACGTGTGCCT
CGCATCTGATGGTGGTGACTCTGCTGTTTGGGACAGCCCTTTTCGTGTACTTGCGACCCAG
CTCCAGCTACTTGCTAGGCAGGGACAAGGTGGTGTCTGTTTTCTATTTCATTGGTGATCCCC
ATGCTGAACCTCTCATTTACAGTTTGAGGAACAAAGAGATCAAGGATGCCCTGTGGAAG
GTGTTGGAAGGAAGAAAGTGTTCCTTAG (SEQ ID NO: 308)

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AOLFR168 sequences:

MEKINNVTETIFWGLSQSPEIEKVCFVVSFFYIHILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV
DICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAYDRYVAICKPLHYM
TIMNRETCKNMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCDVHPVLKLACTETYIVG
25 VVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVIFFGPCTFMYMRPD
TTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO:
309)

30 ATGGAAAAAATAAACAACGTAACCTGAATTCAATTTCTGGGGTCTTTCTCAGAGCCCAGAGA
TTGAGAAAGTTTGTGTTTGTGGTGTTCCTTCTTCTACATAATCATTCTTCTGGGAAATCTC
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTTAAAGTCACCCATGTATTTCTTTCTCAG
CTTCTTGTCTTTTGTGGACATTTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC
TGTTAGCAAAGGACAAAACCATCTCCTTATGTGGGGTGCATGTTGCAACTGCTTGGAGTAC
ATTTCTTTGGTTGCACTGAGATCTTCATCCTTACTGTAATGGCCTATGATCGTTATGTGGCT
35 ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT
TAGGGACGTGGGTAGGTGGGTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAACCT
ACCTTTTGTGGACCCAATGAGATAGATCACTACTTTTGTGATGTTACCCCTGTGTTGAAA
CTTGCTGCACAGAAACATACATTGTTGGTGTGTTGTGACAGCCAACAGTGGTACCATTG
CTCTGGGGAGTTTGTATCTTGCTAATCTCCTACAGCATCATCCTAGTTTCCCTGAGAAAG
40 CAGTCAGCAGAAGGCAGGCGCAAAGCCCTCTCCACCTGTGGCTCCACATTGCCATGGTCG
TTATCTTTTTCGGCCCCGTGACTTTTATGTACATGCGCCCTGATACGACCTTTTCAGAGGAT
AAGATGGTGGCTGTATTTTACACCATTATCACTCCCATGTTAAATCCTCTGATTTATACACT
GAGAAATGCAGAAGTAAAGAATGCAATGAAGAACTGTGGGGCAGAAATGTTTTCTTGGA
GGCTAAAGGGAAATAG (SEQ ID NO: 310)

45

AOLFR169 sequences:

MMDNHSSATEFHLLGFPGSQGLHHILFAIFFFFYLVTLMGNTVIIIVVCVDKRLQSPMYFFLSHL
STLEILVTTHIVPMMLWGLLFLGCRQYLSLHVSLNFSCGTMEFALLGVMAVDRYVAVCNPLRY
NIIMNSSTCIWVIVSWVFGFLSEIWPIYATFQFTFRKSNSLDHFYCDRGQLKLSCDNTLLTEFI
50 LFLMAVFILIGSLIPTIVSYTYIISTILKIPSASGRRKAFSTFASHFTCVVIGYGSCFLFYVKPKQTQ
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDGMKRCCQLLKD (SEQ ID NO: 311)

ATGATGGACAACCACTCTAGTGCCACTGAATTCCACCTTCTAGGCTTCCCTGGGTCCCAAG
GACTACACCACATTCTTTTGTCTATATTCTTTTCTTCTATTAGTGACATTAATGGGAAAC
55 ACGGTCATCATTGTGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCT
CAGCCACCTCTCTACCCTGGAGATCCTGGTCACAACCATAATTGTCCCCATGATGCTTTGG

GGATTGCTCTTCCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCCTG
TGGGACCATGGAGTTTGCATTACTTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTGT
AACCCTTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTTGGGTGGTAATAGTGT
CATGGGTGTTTGGATTTCTTTCTGAAATCTGGCCCATCTATGCCACATTTACGTTTACCTTC
5 CGCAAATCAAATTCATTAGACCATTTTACTGTGACCGAGGGCAATTGCTCAAACGTGCCT
GCGATAACACTCTTCTCACAGAGTTTATCCTTTTCTTAATGGCTGTTTTTATTCTCATTGGT
TCTTTGATCCCTACGATTGTCTCCTACACCTACATTATCTCCACCATCCTCAAGATCCCGTC
AGCCTCTGGCCGAGGAAAGCCTTCTCCACTTTTGCCTCCCACTTCACCTGTGTGTGATTG
GCTATGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACACAGGGAGTTGAGTACAA
10 TAAGATAGTTTCCCTGTTGGTTTCTGTGTTAACCCCTTCCTGAATCCTTTTACTCTTTACTCT
TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCCT
GAAAGATTAG (SEQ ID NO: 312)

AOLFR170 sequences:

15 MSFTSLIPSLCFSLTLPFLFCYLSLLPFLSAFLFITRWLLAFLSLFSVSVPVSSVSSSMVLCYLSVS
ASPSVFCFSCMQGPILWIMANLSQPSEFVLLGFSSFGELQALLYGPFLMLYLLAFMGNTIIIVMVI
ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSDLLVPHKVITFTGCMVQFYFHFSLGSTSFLIL
TDMALDRFVAICHPLRYGTLMSRAMCVQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH
FFCDNEPLLQLSCSDTRLLEFWDFLMLTFLVSSFLVTLISYGYIVTTVLRIPSASSCQKAFSTCG
20 SHLTLVFIGYSSTIFLYVRPGKAHSVQVRKVVALVTSVLTPFLNPFILTFCNQTVKTVLQGMQ
RLKGLCKAQ (SEQ ID NO: 313)

ATGTCTTTCACTTCTCTCATACCCTCACTCTGTTTCTCCTTGACTCTCCCATTCCTGTTTTGT
TATCTTTCTTTATTGCCGTTTCTTTCTGCTTTTCTGTTTATCACTCGCTGGCTACTTGCCTTT
25 CTCTCTCTATTCTCTGTCTGTCCCTGTTTCTCTGTTTCAAGTTCAATGGTTCTCTGTCTC
TATCTCTCTGTTTCTGCCTCTCCGTCTGTCTTTTGTCTCTTGATGCAGGGCCCCATACTG
TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGCTCTTGGGCTTCTCCTCCTTTGG
TGAGCTGCAGGCCCTTCTGTATGGCCCTTCTCATGCTTTATCTTCTCGCCTTCATGGGAA
ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTACTTCTTC
30 CTGGGCAATTTTCCCTGCTGGAGATCTTGGTAACCATGACTGCAGTGCCAGGATGCTCT
CAGACCTGTTGGTCCCCCACAAGTCATTACCTTCACTGGCTGCATGGTCCAGTTCTACTTC
CACTTTTCCCTGGGGTCCACCTCCTTCCTCATCCTGACAGACATGGCCCTTGATCGCTTTGT
GGCCATCTGCCACCCACTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGTCCAGCTG
GCTGGGGCTGCCTGGGCAGCTCCTTTTCTAGCCATGGTACCCACTGTCCTCTCCCGAGCTC
35 ATCTTGATTACTGCCATGGCGACGTCATCAACCATTCTTCTGTGACAATGAACCTCTCCTG
CAGTTGTCACTGTCTGACATCGCTGTTGGAATTCTGGGACTTTCTGATGGCCTTGACCTT
TGTCTCAGCTCCTTCTCCTGGTGACCTCATCTCCTATGGCTACATAGTGACCACCTGTGCTG
GGATCCCCTCTGCCAGCAGCTGCCAGAAGGCTTTCTCCACTTGCGGGTCTCACCTCACT
GGTCTTCATCGGCTACAGTAGTACCATCTTTCTGTATGTGAGGCCTGGCAAAGCTCACTCT
40 GTGCAAGTCAGGAAGGTCGTGGCCTTGGTGACTTCAGTTCTCACCCCTTTCTCAATCCCT
TTATCCTTACCTTCTGCAATCAGACAGTTAAACAGTGCTACAGGGGCAGATGCAGAGGCT
GAAAGGCCTTTGCAAGGCACAATGA (SEQ ID NO: 314)

AOLFR171 sequences:

45 MVGNLLIWVTITIGSPSLGSLMYFFLAYLSLMDAIYSTAMSPKLMIDLCDKIAISLSACMGQLFI
EHLGGAEVFLLVVMAYDRYVAISKPLHYLNIMNRLVCILLVVAMIGGFVHSVQIVFLYSLP
ICGPNVIDHSVCDMYPLLELLCLDTYFIGLTVVANGGICMVIFTFLLISCGVILNFKTYSQEER
HKALPTCISHIIVVALVFVPCIFMYVRPVSNNFPDKLMTVFYSIITLMLNPLIYSLRQSEMKNAM
KNLWCEKLSIVRKRVSPTLNIFIPSSKATNRR (SEQ ID NO: 315)

50 ATGGTGGGAAACCTCCTCATTGTTGGGTGACTACTATTGGCAGCCCTCCTTGGGCTCCCTAA
TGTAATCTCTCCTTGCTACTTGTCACTTATGGATGCCATATATTCCACTGCCATGTCAACC
AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTTCTTGTGAGCTTGCATGGGTC
AGCTCTTCATAGAACACTTACTTGGTGGTGCAGAGGTCTTCCTTTTGGTGGTGATGGCCTA
55 TGATCGCTATGTGGCTATCTCTAAGCCGCTGCACTATTTGAACATCATGAATCGACTGGTT
TGCATCCTTCTGTTGGTGGTGGCCATGATTGGAGGTTTTGTGCACTCTGTGGTTCAAATTGT

CTTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT
ACCCATTGTTGGAAGTGTGTGCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA
TGGTGGGAATAATTTGTATGGTCATCTTTACCTTTCTGCTAATCTCCTGTGGAGTCATCCTAA
ACTTCCTTAAAACTTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCCA
5 CATCATTGTGGTTGCCCTCGTTTTTGTTCCTGTATTTTTATGTATGTTAGACCCGTTTCCA
ACTTTCCCTTTGATAAAATTAATGACTGTGTTTTATTCAATTATCACACTCATGTTGAATCCT
TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA
AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCACACTGAACATATTTATTCCTAGTTCTA
AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

10

AOLFR172 sequences:

MAETLQLNSTFLHPNFFILTGFPGLGSAQTWLTFLVFGPIYLLALLGNGALPAVVWIDSTLHQPM
FLLLAILAATDLGLATSIAPGLLAVLWLGPRSVPYAVCLVQMFFVHALTAMESGVLLAMACDR
AAAIGRPLHYPVLVKACVGYAALALALKAVAIVVPFLLVAKFEHFQAKTIGHTYCAHMAV
15 VELVVGNTQATNLYGLALSLAISGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSSHCIVL
AFYIPGLFSYLAHRFGHHTVPKPVHILLSNIYLLPPALNPLIYGARTKQIRDRLLETFTFRKSPL
(SEQ ID NO: 317)

20

ATGGCAGAACTCTACAACCTCAATTCCACCTTCCTACACCCAACTTCTTCATACTGACTG
GCTTTCCAGGGCTAGGAAGTGCCAGACTTGGCTGACACTGGTCTTTGGGCCCATTTATCT
GCTGGCCCTGCTGGGCAATGGAGCACTGCCGGCAGTGGTGTGGATAGACTCCACACTGCA
CCAGCCCATGTTTCTACTGTTGGCCATCCTGGCAGCCACAGACCTGGGCTTAGCCACATCT
ATAGCCCCAGGGTTGCTGGCTGTGCTGTGGCTTGGGCCCCGATCTGTGCCATATGCTGTGT
GCCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC
25 CATGGCCTGTGATCGTGCTGCGGCAATAGGGCGTCCACTGCACTACCCTGTCCTGGTCACC
AAAGCCTGTGTGGGTTATGCAGCCTTGGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC
CTTTCCCACTGCTGGTGGCAAAGTTTGAGCACTTCCAAGCCAAGACCATAGGCCATACCTA
TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGGTAACACACAGGCCACCAACTTATA
TGGTCTGGCACTTTCACTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT
GGACTCATTGCCCATGCTGTGCTGCAGCTACCTACCCGGGAGGCCCATGCCAAGGCCTTTG
30 GTACATGTAGTTCTCACATCTGTGTCATTCTGGCCTTCTACATACCTGGTCTCTTCTCCTAC
CTCGCACACCGCTTTGGTCATCACACTGTCCCAAAGCCTGTGCACATCCTTCTCTCCAACAT
CTACTTGCTGCTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCGCACCAAGCAGATC
AGAGACCGACTCCTGGAAACCTTCACATTCAGAAAAAGCCCGTTGTAA (SEQ ID NO: 318)

35

AOLFR173 sequences:

MSHTNVTIFHPAVFVLPGIPGLEAYHIWLSIPLCLYITAVLGNSILIVVIVMERNLHVPMYFFLS
MLAVMDILLSTTTVPKALAIFWLQAHNIAFDACVTQGGFFVHMMFVGESAILLAMAFDRFVAIC
APLRYTTVLTPVVGRIALAVITRSFCIIFVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV
40 NIWYGFSPVIVMVILDVILIAVSYSLLRAVFRLPDARHKALSTCGSHLCVILMFYVPSFFTLL
THHFGRNIPQHVHILLANLYVAVPPMLNPVYGVKTKQIREGV AHRFFDIKTWCCTSPLGS
(SEQ ID NO: 319)

45

ATGAGTCACACCAATGTTACCATCTTCCATCCTGCAGTTTTTGTCTTCTCCTGGCATCCCTGG
GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTTGCCTCATTTACATCACTGCAGTCC
TGGGAAACAGCATCCTGATAGTGTTATTGTCATGGAACGTAACCTTCATGTGCCCATGTA
TTTCTTCTCTCAATGCTGGCCGTGATGGACATCCTGCTGTCTACCACCACTGTGCCCAAGG
CCCTAGCCATCTTTTGGCTTCAAGCACATAACATTGCTTTTGATGCCTGTGTACCCAAAGGC
TTCTTTGTCCATATGATGTTTGTGGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATCG
50 CTTTGTGGCCATTTGTGCCCCACTGAGATATACAACAGTGCTAACATGGCCTGTTGTGGGG
AGGATTGCTCTGCGCCGTATCACCCGAAGCTTCTGCATCATCTTCCCAGTCATATTCTTGCT
GAAGCGGCTGCCCTTCTGCCTAACCAACATTGTTTCTCCTCACTCCTACTGTGAGCATATTGGA
GTGGCTCGTTTAGCCTGTGCTGACATCACTGTAAACATTTGGTATGGCTTCTCAGTGCCCAT
TGTCATGGTCATCTTGGATGTTATCCTCATCGCTGTGCTTACTCACTGATCCTCCGAGCAG
55 TGTTTCGTTTGGCCTCCAGGATGCTCGGCACAAGGCCCTCAGCACTTGTGGCTCCACCT
CTGTGTCATCCTTATGTTTTATGTTCCATCCTTCTTTACCTTATTGACCCATCATTTTGGGCG

TAATATTCCTCAACATGTCCATATCTTGCTGGCCAATCTTTATGTGGCAGTGCCACCAATGC
TGAACCCCATTTGTCTATGGTGTGAAGACTAAGCAGATACGTGAGGGTGTAGCCACCGTT
CTTTGACATCAAGACTTGGTGTGTACCTCCCCTCTGGGCTCATGA (SEQ ID NO: 320)

5 **AOLFR175 sequences:**

MHFLSQNDLNINLIPHLCLHRHSVIAGAFTIHRHMKIFNSPSNSSTFTGFILLGFPCPREGQILLFV
LFTVVYLLTLMGNGSIICAVHWDQRLHAPMYILLANFSFLEICYVTSTVPSMLANFLSDTKIISF
SGCFLQFYFFFSLGSTECFFLA VMAFDRYLAICRPLRYPTIMTRRLCTNLVVNCWVLGFIWFLPI
VNISQMSFCGSRIIDHFLCDPAPLLTLTCKKGPVIELVFSVLSPLPVFMLFLFIVGSYALVVRAVL
10 RVPSAAGRRAKAFSTCGSHLAVVSLFYGSVLVVMYGSPPSKNEAGKQKTVTLFYSVVTPLLNPVI
YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTTCCCAAAATGATTTAAATATAAAATCTGATTCCCCATCTATGTTTGCACCG
TCATTAGTAATTGCTGGTGCTTTTACAATTCACAGGCACATGAAAATCTTCAACAGCCCC
15 AGCAACTCCAGCACCTTCACTGGCTTCATCCTCCTGGGCTTCCCTTGCCCCAGGGAGGGGC
AGATCCTCCTCTTTGTGCTCTTCACTGTTGTTTACCTCCTGACCCTCATGGGCAATGGTTCC
ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCCTGCTCGCCA
ACTTCTCCTTCTTGAGATATGTTATGTCACCTCCACAGTCCCAGCATGCTGGCCAACTTC
CTCTCTGACACCAAGATCATCTCGTTCTCTGGCTGCTTCCCTCCAGTTCTACTTTTCTTCTCC
20 TTGGGCTCTACAGAATGCTTTTCCCTGGCAGTTATGGCATTGATCGATACCTTGCCATCTG
TCGGCCTCTACGCTATCCAACCATTATGACCAGACGCTCTGTACCAATCTTGTGGTCAATT
GCTGGGTACTTGGTTTCATCTGGTTCTTGATTCCTATCGTCAACATCTCCCAAATGTCCTTC
TGTGGATCTAGGATTATTGACCACTTCCTATGTGACCCAGCTCCTCTTCTAACTCTCACTTG
CAAAAAGGCCCTGTGATAGAGCTTGCTTTTCTGTCTTAAGTCTCTGCCTGTCTTTATGC
25 TCTTTCTCTTCAATTGTGGGTCTATGCTCTGGTGTGAGAGCTGTGTTGAGGGTCCCTTCA
GCAGCTGGGAGAAGAAAGGCTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCCACCATCTAAGAATGAAGCTGGAAGC
AGAAGACTGTGACTCTGTTTTATTCTGTTGTTACCCACTGCTTAACCCTGTGATATATAGT
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTGGGGAACATAA (SEQ ID NO:
30 322)

AOLFR176 sequences:

MFFIIHSLVTSVFLTALGPQNRTMHFVTEFVLLGFHGQREMQSCFFSFILVLYLLTLGNGAIVC
AVKLDRLHTPMYILLGNFAFLEIWIYISSTVPNMLVNILSEIKTISFSGCFLQFYFFFSLGTECFE
35 LSV MAYDRYLAICRPLHYPSIMTGKFCILVCVCWVGGFLCYPVPIVLISQLPFCGPNIIDHLVCD
PGPLFALACISAPSTELICYTFNSMIIFGPFLSILGSYTLVIRAVLCIPSGAGRTKAFSTCGSHLMV
VSLFYGTLMVMYVSPTSGNPAGMQKIITLVYTAMTPFLNPLIYSLRNKDMKDALKRVLGLTVS
QN (SEQ ID NO: 323)

ATGTTCTTTATTATTCACTTCTTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCAGAA
CAGAACAATGCATTTTGTGACTGAGTTTGTCTCCTGGGTTTCCATGGTCAAAGGGAGATG
CAGAGCTGCTTCTTCTCATTCACTCCTGGTTCTCTATCTCCTGACACTGCTAGGGAATGGAGC
TATTGTCTGTGCAGTGAAATTGGACAGGCGGCTCCACACACCCATGTACATCCTTCTGGGA
AACTTTGCCTTTCTAGAGATCTGGTACATTTCCTCCACTGTCCCAAACATGCTAGTCAATAT
45 CCTCTCTGAGATTA AAAACCATCTCCTTCTCTGGTTGCTTCTGCAATTCTATTTCTTTTTTC
ACTGGGTACAACAGAGTGTTTCTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC
TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTGT
ATGCTGGGTAGGCGGATTTCTCTGCTATCCAGTCCCTATTGTTCTTATCTCCCAACTTCCCT
TCTGTGGGCCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCCATGTTTGCCTGGC
50 CTGCATCTCTGCTCCTTCCACTGAGCTTATCTGTTACACCTTCAACTCGATGATTATCTTTG
GGCCTTCCCTCTCCATCTTGGGATCTTACACTCTGGTCATCAGAGCTGTGCTTTGTATTCCC
TCTGGTGCTGGTCAACTAAAGCTTTCTCCACATGTGGGTCCACCTAATGGTGGTGTCTC
TATTCTATGGAACCTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT
GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTTAAATCCCTTATCTAT
55 AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCTGGGGTTAACAGTTAGC
CAAACTGA (SEQ ID NO: 324)

[illegible]

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ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTCATGGGACTCACCAACTCAC
 GGGAGATTGAGCTTCTACTTTTTGTTTTCTCTTTGTTGTTCTACTTTGCGAGCATGATGGGA
 AACCTTGTCATTGTATTCAGTGAACCATGGATGCTCATCTGCACTCCCCCATGTATTTCT
 5 CCTGGCTAACCTCTCAATCATTGATATGGCATTGTTGCTCAATTACAGCCCCTAAGATGATTT
 GTGATATTTTCAAGAAGCACAAGGCCATCTCCTTTCGGGGATGTATTACTCAGATCTTCTT
 TAGCCATGCTCTTGGGGGCACTGAGATGGTGTCTCATAGCCATGGCCTTTGACAGATAC
 ATGGCCATATGTAAACCTCTCCACTACCTGACCATCATGAGCCCAAGAATGTGTCTATACT
 TTTTAGCCACTTCTCTATCATTGGCCTTATCCACTCATTGGTCCAATTAGTTTTTGTGGTA
 10 GATTTACCTTTTTGTGGTCTTAATATCTTTGACAGTTTTTACTGTGATCTCCCTCGGCTCCT
 CAGACTTGCTGTACCAACACCCAAGAAGTGGAGTTCATGGTCACTGTCAATAGTGGACTC
 ATTTCTGTGGGCTCCTTTGTCTTGTCTGTAATTTCTACATCTTCATTCTGTTCAGTGTG
 GAAACATTCTTCTGGTGGTCTAGCCAAAGGCCCTCTCTACCCTGTCAGCTCATGTCTG
 GTCATCTTGTCTTTGGGCCACTGATGTTTTTCTACACATGGCCTTCTCCACATCACACCT
 15 GGATAAATATCTTGCTATTTTTGATGCATTTATTACTCCTTTTCTGAATCCAGTTATCTACA
 CATTGAGGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCAGTCGTCTTGCGCATT
 TTACAAAGATTTTGTA (SEQ ID NO: 330)

AOLFR180 sequences:

20 MTNKMAYAIYIKNLNYFSLIVQCLQPTMAIFNNTTSSSSNFLLTAFPGLECAHVWISIPVCCLYTI
 ALLGNSMIFLVIITKRRLHKPMYYFLSMLAAVDLCLTITLPTVLGVLFHAREISFKACFIQMF
 FVHAFSLLESSVLVAMAFDRFVAICNPLNYATILTDRMVLVIGLVICIRPAVFLPLLVAINTVSF
 HGGHELSPFCYHPEVIKYTYSKPWISFWGLFLQLYLNGLDVLFILFSYVLILRTVLGIVARKK
 QQKALSTCVCHICAVTIFYVPLISLSLAHRLFHSTPRVLCSTLANIYLLLPPVLNPIIYSLKTKTIR
 25 QAMFQLLQSKGSWGFNVRGLRGRWD (SEQ ID NO: 331)

ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTTCTTTCCTCATAGT
 TCAGTGTCTTCAACCAACCATGGCAATATTCAATAACACCACTTCGTCTTCTCAAACCTTCC
 TCTCACTGCATTCCCTGGGCTGGAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT
 30 CTCTACACCATTGCCCTCTTGGGAAACAGTATGATCTTTCTTGTCTCATTTACTAAGCGGA
 GACTCCACAAACCCATGTATTATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC
 ATTACGACCTTCCCACTGTGCTTGGTGTCTCTGTTTCATGCCCGGGAGATCAGCTTTAA
 AGCTTGCTTCATTCAAATGTTCTTTGTGCATGCTTTCTCCTTGCTGGAGTCCCTCGGTGCTGG
 TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCCACTGAACTATGCTACTATCCTC
 35 ACAGACAGGATGGTCTGGTGATAGGGCTGGTCATCTGCATTAGACCAGCAGTTTTCTTAC
 TTCCCCTTCTTGTAGCCATAAACACTGTGTCTTTTCATGGGGGTCACGAGCTTTCCCATCCA
 TTTTGCTACCACCCAGAAGTGATCAAATACACATATTCCAAACCTTGGATCAGCAGTTTTT
 GGGGACTGTTTCTTCACTCTACCTGAATGGCACTGACGTATTGTTTATTCTTTCTCCTAT
 GTCCTGATCCTCCGTACTGTTCTGGGCAATTGTGGCCGAAAGAAGCAACAAAAAGCTCTCA
 40 GCATTGTGCTGTGCATCTGTGCAGTCACTATTTCTATGTGCCACTGATCAGCCCTCTCT
 TTGGCACACCGCTCTTCCACTCCACCCCAAGGGTGCTCTGTAGCACTTTGGCCAATATTTA
 TCTGCTCTTACCACCTGTGCTGAACCCTATCATTTACAGCTTGAAGACCAAGACAATCCGC
 CAGGCTATGTTCCAGCTGCTCCAATCCAAGGGTTCATGGGGTTTTAATGTGAGGGGTCTTA
 GGGGAAGATGGGATTGA (SEQ ID NO: 332)

AOLFR181 sequences:

MSVLNNSEVKLFLLIGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIKTEPSLHEPMMYYFLAML
 AVSDMGLSLSSLPTMLRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLIMSLDRFLAIHNPLR
 YSSILTSNRVAKMGLILAIRSILLVIPFFTLRLRLKYCQKNLLSHSYCLHQDTMKLACSDNKTNV
 50 IYGFFIALCTMLDLALIVLSYVLILKILSLASLAERLKAALNTCVSHICAVLTFYVPIITLAAMHHF
 AKHKSPLVVILIADMFLLVPLMNPVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCTTCTGATTGGGATCCCAGGACTGG
 AACATGCCACATTTGGTTCTCCATCCCCATTTGCCTCATGTACCTGCTTGCCATCATGGGC
 55 AACTGCACCATTTCTTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATTT
 CCTTGCCATGTTGGCTGTCTCTGACATGGGCCTGTCCCTCTCCTCCCTTCCCTACCATGTTGA

GGGTCTTCTTGTTC AATGCCATGGGAATTTACCTAATGCCTGCTTTGCTCAAGAATTCTTC
 ATTCATGGATTCACTGTCATGGAATCCTCAGTACTTCTAATTATGTCTTTGGACCGCTTTCT
 TGCCATTCACAATCCCTTAAGATACAGTTCTATCCTCACTAGCAACAGGGTTGCTAAAATG
 GGACTTATTTTAGCCATTAGGAGCATTCTCTTAGTGATTCCATTCCCTTCACCTTAAGGAG
 5 ATTAAAATATTGTCAAAAAGAATCTTCTTTCTCACTCATACTGTCTTCATCAGGATACCATGA
 AGCTGGCCTGCTCTGACAACAAGACCAATGTCATCTATGGCTTCTTCATTGCTCTCTGTACT
 ATGCTGGACTTGGCACTGATTGTTTTGTCTTATGTGCTGATCTTGAAGACTATACTCAGCAT
 TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGTCTCCCACATCTGTGCTGTG
 CTCACCTTCTATGTGCCCATCATCACCTGGCTGCCATGCATCACTTTGCCAAGCACAAAA
 10 GCCCTCTTGTGTGATCCCTTATTGCAGATATGTTCTTGTGTTGGTGCCGCCCTTATGAACCCC
 ATTGTGTACTGTGTAAAGACTCGACAAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAAT
 GTATGTGGGAGATAA (SEQ ID NO: 334)

AOLFR182 sequences:

15 MTLGSLGNSSSSVSATFLLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIKTERSLHEPMYLFL
 SMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFFIHCFSFLESSVLLSMAFDRFVAICHP
 LHYVSILTNTVIGRIGLVSIGRSVALIFPLPFMLKRFPCGSPVLSHSYCLHQEVMKLACADMK
 ANSIYGMFVIVSTVGIDSLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV
 IHRFGKQAPHLVQVVMGMFYLLFPVPMNPVYSVKTKQIRDRVTHAFCY (SEQ ID NO: 335)

20 ATGACCCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCCTGCTGAGTG
 GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCCTGTGCTTCATGTATCT
 GGTTTCCATCCCGGGCAACTGCACAATTCTTTTATCATTAAAACAGAGCGCTCACTCAT
 GAACCTATGTATCTCTTCTGTCCATGTGCTGGCTCTGATTGACCTGGGTCTCTCCCTTTGCAC
 25 TCTCCCTACAGTCTCTGGGCATCTTTTGGGTGGAGCAGCAGAAATTAGCCATGATGCCTGC
 TTTGCTCAGCTCTTTTTCATTCACTGCTTCTCTTCTCGAGTCTCTGTGCTACTGTCTATG
 GCCTTTGACCGCTTTGTGGCTATCTGCCACCCCTTGCACTATGTTCCATTCTCACCAACAC
 AGTCATTGGCAGGATTGGCCTGGTCTCTCTGGGTCGTAGTGTAGCACTCATTTTCCATTA
 CCTTTTATGCTCAAAAGATTCCCCTATTGTGGCTCCCCAGTTCTCTCACATTCTTATTGTCT
 30 CCACCAAGAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT
 GTTTGTCATCGTCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTCTTATGCTCTGA
 TCCTGCGCACCGTGCTGTCCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG
 TGTTTCCACATCTGTGCTGTGCTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTCTATCC
 ATCGCTTTGGAAAGCAGGCACCCACCTGGTCCAGGTGGTCATGGGTTTCATGTATCTTCT
 35 CTTTCTCTGTGATGAATCCCATTGTCTACAGTGTGAAGACCAAACAGATCCGGGGATCGA
 GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

AOLFR183 sequences:

40 MTNLNASQANHRNFILTGIPGTPDKNPWLAFLPLGFLYTLTLLGNGTILAVIKVEPSLHEPTYFYFL
 SILALTDVLSMSLPSMLSIYWFNAPQIVFDACIMQMFFIHVFGIVESGVLVSMAFDRFVAIRN
 PLHYVSILTHDVIRKTGISVLTRAVCVVPVFLIKCLPFCHSNVLSHSYCLHQNMMLACASTR
 INSLYGLIVIFTLGLDVLLTLLSYVLTLKTVLGIVSRGERLKLSTCLSHMSTVLLFYVPMGA
 ASMIHRFWEHLSPVVHVMADIYLLPPVLNPVYSVKTKQI (SEQ ID NO: 337)

45 ATGACGAACTTGAATGCATCACAGGCCAACACCGTAACTTCATTCTGACAGGTATCCCAG
 GAACGCCAGACAAGAACCCATGGTTGGCCTTTCCCCTGGGATTTCTCTACACACTCACT
 CCTGGGAAATGGTACCATCCTAGCTGTCATCAAGGTGGAGCCAAGTCTCCATGAGCCCACG
 TATTACTTCCTTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCCTCC
 ATGCTCAGCATCTACTGGTTTAATGCCCTCAGATTGTTTTGATGCATGCATCATGCAGAT
 50 GTTCTTCATCCATGTATTTGGAATAGTAGAATCAGGAGTCCTAGTGCCATGGCCTTTGAC
 AGATTTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTCAGATGTTATTCCG
 AAAGACTGGAATATCTGTCTCACCCGGGCACTGTGTGGTATTCCCTGTGCCCTTCCTT
 ATAAAGTGCCCTACCCTTCTGCCATTCCAATGTCTTGTCTCATTCACTGTCTTACCAAAA
 CATGATGCGGCTAGCTTGTGCCAGCACCCGCATCAACAGCCTCTACGGCCTCATCGTCGTC
 55 ATCTTCACACTGGGGCTCGATGTTCTCTCACTCTACTGTCTTATGTACTCACCTGAAGAC
 TGTGCTGGGCATTGTCTCCAGAGGTGAAAGGCTGAAAACCCCTCAGCACATGCCTCTCTCAC

ATGTCTACCGTGCTCCTCTTCTATGTTCTTTTATGGGTGCTGCCTCCATGATCCACAGATT
TTGGGAGCATTATACACCAGTAGTGCACATGGTCATGGCTGATATATACCTACTGCTCCCG
CCTGTGCTAAACCCCATGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

5 **AOLFR184 sequences:**

MSTLPTQIAPNSSTSMAPTFLVGMPLSGAPSWWTLPLIAVYLLSALGNGTILWIIALQPALHR
PMHFFLFLSVSDIGLVTALMPTLLGIALAGAHTVPASACLLQMVFIHVFSVMESSVLLAMSID
RALAICRPLHYPALLTNGVISKISLAISFRCLGLHLPLPFLAYMPYCLPQVLTHSYCLHPDVARL
ACPEAWGAAYSFLVLSAMGLDPLLIFFSYGLIGKVLQGVESREDRWKAGQTCAHLSAVLLF
YIPMILLALINHPITQHTHTLLSYVHFLPLINPILYSVKMKEIRKRLNRLQPRKVGGAAQ
(SEQ ID NO: 339)

15 ATGTCAACATTACCAACTCAGATAGCCCCCAATAGCAGCACTTCAATGGCCCCCACCTTCT
TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCCTCCTGGTGGACATTGCCCTCATTGC
TGTCTACCTTCTCTCTGCACTGGGAAATGGCACCATCCTCTGGATCATTGCCCTGCAGCCC
GCCCTGCACCGCCCAATGCACTTCTTCTCTTCTGCTTAGTGTGTCTGATATTGGATTGGT
CACTGCCCTGATGCCACACTGCTGGGCATCGCCCTGCTGGTGTCTACACTGTCCCTGCC
TCAGCCTGCCTTCTACAGATGGTTTTATCCATGTCTTTTCTGTCTATGGAGTCTCTGTCTT
GCTCGCCATGTCCATTGATCGGGCACTGGCCATCTGCCGACCTCTCCACTACCCAGCGCTC
20 CTCACCAATGGTGTAAATTAGCAAAATCAGCCTGGCCATTTCTTTTCGATGCCTGGGTCTCC
ATCTGCCCCTGCCATTCTGCTGGCCTACATGCCCTACTGCCTCCCACAGGTCTTAACCCAT
TCTTATTGCTTGCATCCAGATGTGGCTCGTTTGGCCTGCCAGAAGCTTGGGGTGCAGCCT
ACAGCCTATTTGTGGTCTTTTCAGCCATGGGTTTGGACCCCTGCTTATTTTCTTCTCTAT
GGCCTGATTGGCAAGGTGTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGCTGGT
25 CAAACCTGTGCTGCCACCTCTCTGCACTGCTCCTCTTCTATATCCCTATGATCCTCCTGGC
ACTGATTAACCATCCTGAGCTGCCAATCACTCAGCATACCCATACTCTTCTATCCTATGTCC
ATTTCTTCTTCTCCTCCATTGATAAACCTATTCTCTATAGTGTCAAGATGAAGGAGATTAGA
AAGAGAATACTCAACAGGTGTCAGCCAGGAAGGTGGGTGGTGTCTCAGTGA (SEQ ID NO:
340)

30 **AOLFR185 sequences:**

MFYPILNDISTKNNSNIMSCCNILFIKTVEIILVYNQTQSPWYPIVPSKSLVYNNNTCFDCYHLQR
VDCVPSRDHINQSMVLASGNSSHPVSFILLGIPGLESFQLWIAFPFCATYAVAVVGNITLLHVIR
IDHTLHEPMYLFLAMLAITDLVLSSTQPKMLAIFWFHAHEIQYHACLIQVFFIHAFSSVESGVL
35 MAMALDCYVATCFPLRHSSILTPSVVIKLTIVMLRGLLWVSPFCFMVSRMPFCQHQAIPQSYC
EHMAVLKLVCADTSISRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA
SHICVILALYIPALFSFLTYRFGHDVPRVVHILFANLYLLIPMLNPIHYGVRTKQIGDRVIQGCCG
NIP (SEQ ID NO: 341)

40 ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTCTGTT
GTAACATATTATTTATTAACAGTTGAAATTATTCTAGTTTATAATCAAACCCAATCACC
CTGGTATCCAATAGTCCCATCCAAAAGCCTTGATATAATAATAACACTGTTTTGATTGTT
ATCATCTGCAGAGAGTAGATTGCGTTCACGAGAGACCATATTAACAGTCCATGGTGTCT
GGCTTCAGGGAACAGCTCTTCTCATCCTGTGTCTTCTCATCCTGCTTGGAAATCCAGGCCTG
45 GAGAGTTTCCAGTTGTGGATTGCCTTTCCGTTCTGTGCCACGTATGCTGTGGCTGTTGTGG
AAATATCACTCTCCTCCATGTAATCAGAATTGACCACACCCTGCATGAGCCCATGTACCTC
TTTCTGGCCATGCTGGCCATCACTGACCTGGTCTCTCTCCTCCTCACTCAACCTAAGATGTT
GGCCATATTCTGGTTTCATGTCTCATGAGATTGACATGCTGCCTGCCTCATCCAGGTGTTCT
TCATCCATGCCTTTTCTTCTGTGGAGTCTGGGGTGTCTATGGCTATGGCCCTGGACTGTCTAC
50 GTGGCTACCTGCTTCCCACTCCGACACTCTAGCATCCTGACCCCATCGGTGCTGATCAAAC
TGGGGACCATCGTGATGCTGAGAGGGCTGCTGTGGGTGAGCCCTTCTGCTTCATGGTGTCT
TAGGATGCCCTTCTGCCAACACCAAGCCATTCCCCAGTCATACTGTGAGCACATGGCTGTG
CTGAAGTTGGTGTGTGCTGATACAAGCATAAGTCGTGGGTATGGGCTCTTTGTGGCCTTCT
CTGTGGCTGGCTTTGATATGATTGTCTATGGTATGTCATACGTGATGATTTTGAGAGCTGT
55 GCTTCAGTTGCCCTCAGGTGAAGCCCGCCTCAAAGCTTTTAGCACACGTGCCTCCCATATC
TGTGTCTCTTGGCTCTTTATATCCAGCCCTTTTTCTTCTCACCTACCGCTTTGGCCAT

GATGTGCCCCGAGTTGTACACATCCTGTTTGCTAATCTCTATCTACTGATACCTCCCATGCT
CAACCCCATCATTTATGGAGTTAGAACCAAACAGATCGGGGACAGGGTTATCCAAGGATG
TTGTGGAACATCCCCTGA (SEQ ID NO: 342)

5 **AOLFR186 sequences:**

MSNASLVTAFILTGPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAIISYPL
RYTSMMSGSRCALLATGTWLSGSLHSAVQTILTFHLPYCGPNQIQHYFCDAPPILKLACADTSA
NVMVIFVDIGIVASGCFVLIVLSYVSIVCSILRIRTS DGRRRAFQTCASHCIVVLCFFVPCVVIYLR
10 PGSMAMDGVVAIFYTVLTPLLNPVVYTLRNKEVKKAVLKL RDKVAHPQRK (SEQ ID NO:
343)

ATGTCCAACGCCAGCCTCGTGACAGCATTATCCTCACAGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCTCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
15 CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTCCACAGCTGCGTGGCTCAGCTCTATTTTT
TCCACTTCCTGGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCCTATGATCGCTACTTG
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGGTGTGCCCTCCTGG
20 CCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA
AACTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTCATCTTTGTGGACATTGGGATAGT
GGCCTCAGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCTGC
GGATCCGCACCTCAGATGGGAGGCGCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATTGT
25 GGTCTTTGCTTCTTTGTCCCTGTGTTGCTATTATCTGAGGCCAGGCTCCATGGATGCCA
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACGCCCTTCTCAACCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTTAGAGACAAAGTAGCACAT
CCTCAGAGGAAATAA (SEQ ID NO: 344)

30 **AOLFR187 sequences:**

MAQVRALHKIMALFSANSIGAMNNSDTRIAGCFLTGIPGLEQLHIWLSIPFCIMYIAALEGNIL
CVILSQAILHEPMYIFLSMLASADVLLSTTMPKALANLWLGYSHISFDGCLTQKFFIHLFIHSA
VLLAMAFDRYVAICSPRLRYVTILTSKVIKIVTATLSRSFIIMFPSIFLLEHLHYCQINIIAHTFCEH
MGIAHLSCSDISINWYGLAAALLSTGLDIMLITVSYIHILQAVFRLLSQDARSKALSTCGSHICV
35 ILLFYVPALFSVFAYRFGGRSIPCYVHILLASLYVVIPMLNPVIYGVRTKPILEGAKQMFSNLAK
GSK (SEQ ID NO: 345)

ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG
CTATGAACAACCTCTGACACTCGCATAGCAGGCTGCTTCCTCACTGGCATCCCTGGGCTGGA
40 GCAACTACATATCTGGCTGTCCATCCCCTTCTGCATCATGTACATCGCTGCCCTGGAAGGC
AATGGCATCCTAATTTGTGTCATCCTCTCCAGGCAATCCTGCATGAGCCCATGTACATAT
TCTTATCTATGCTGGCCAGTGCTGATGTCTTGCTCTCTACCACCACCATGCCTAAGGCCCTG
GCCAATTTGTGGCTAGGTTATAGCCACATTTCTTTGATGGCTGCCTCACTCAAAAGTTCTT
CATTCATTCTCTTCATTCACTCTGCTGTCTGCTGGCCATGGCCTTTGACCGCTATGTGG
45 CCATCTGCTCCCCCTGCGATATGTCACAATCCTCACAAGCAAGGTCATTGGGAAGATCGT
CACTGCCACCCTGAGCCGCAGCTTCATCATTATGTTTCCATCCATCTTTCTCCTTGAGCACC
TGCATATTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATTGCCCA
TCTGTCTGTTCTGATATCTCCATCAATGTCTGGTATGGGTTGGCAGCTGCTCTCTCTCCA
CAGGCCTGGACATCATGCTTATTACTGTTTCTACATCCACATCCTCCAAGCAGTCTTCCGC
50 CTCCTTTCTCAAGATGCCCGCTCCAAGGCCCTGAGTACCTGTGGATCCCATATCTGTGTCAT
CCTACTCTTCTATGTCCCTGCCCTTTTTCTGCTTTTGCTACAGGTTTGGTGGAAGAAGCA
TCCCATGATGTCATATTCTCTGGCCAGCCTCTACGTTGTCATTCTCCTATGCTCAAT
CCCGTTATTTATGGAGTGAGGACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTTCA
AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

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AOLFR188 sequences:

MFPSLCPCVLLVQLPLMNENMQCFVFCSCDSLRLMMVSRFIHVFPVKMKRIHVGGSYKHFFSN
ELLCVRPWSGKTWSIRHHIFDMELLTNLKFITDPFVCLRLHLSPTPSEEHMKNNKNNVTEFILL
GLTQNPEGQKVLFTVFLIYMVTIMGNLLIIVTIMASQSLGSPMYFFLASLSFIDTVYSTAFAPK
5 MIVDLLSEKKTISFQGCMAQLFMDHLFAGAEVILLVVMAYDRYMAICKPLHELITMNNRVCVL
MLLAAWIGGFLHSLVQFLFIYQLPFCGPNVIDNFLCDLYPLLKLACTNTYVTGLSMIANGGAIC
AVTFFTILLSYGVILHSLKTQSLEGKRKAFYTCASHVTVVILFFVPCIFLYARPNSTFPIDKSMTV
VLTFITPMLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)

10 ATGTTCCCCCTCCCTGTGTCCATGTGTTCTCCTTGTTCAACTCCCCTTATGAATGAGAACAT
GCAGTGTTTTGTTTTCTGTTCTTGTGATAGTTTGCTGAGAATGATGGTTTCCCGCTTCATCC
ATGTCCCATTGTGAAAAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTTC
TAATGAGCTGCTCTGTGTGAGGCCCTGGTCAGGGAAAACGTGGTCGATAAGGCATCACAT
TTTTGACATGGAGCTTCTGACAAATAATCTCAAATTTATCACTGACCCTTTTGTGTGAGGC
15 TCCGACACCTGAGTCCAACACCTTCAGAAGAACACATGAAAAATAAGAACAATGTGACTG
AATTTATCCTCTTAGGGCTCACACAGAACCCTGAGGGGCAAAAAGGTTTTATTTGTCACATT
CTTACTAATCTACATGGTGACGATAATGGGCAACCTGCTTATCATAGTGACCATCATGGCC
AGCCAGTCCCCTGGGTTCCCCCATGTACTTTTTTCTGGCTTCTTTATCATTATAGATACCGT
CTATTCTACTGCATTTGCTCCCAAAATGATTGTTGACTTGCTCTCTGAGAAAAAGACCATT
20 CCTTTCAGGGTTGTATGGCTCAACTTTTTATGGATCATTATTTGCTGGTGCTGAAGTCATT
CTTCTGGTGGTAATGGCCTATGATCGATACATGAGCCATCTGTAAGCCTCTTCATGAATTGA
TCACCATGAATCGTCGAGTCTGTGTTCTTATGCTGTTGGCGGCCTGGATTGGAGGCTTTCT
TCACTCATTGGTTCAATTTCTCTTTATTTATCAGCTCCCTTTCTGTGGACCCAATGTCATTG
ACAACTTCCTGTGTGATTTGTATCCCTTATTGAACTTGCTTGACCAATACCTATGTCATT
25 GGGCTTCTATGATAGCTAATGGAGGAGCGATTTGTGCTGTCACCTTCTTCACTATCCTGC
TTTCTATGGGGTCATATTACACTCTCTTAAGACTCAGAGTTTGGAAGGGAAAACGAAAAGC
TTTCTACACCTGTGCATCCACGTCACCTGTGGTCATTTTATTCTTTGTCCCCTGTATCTTCTT
GTATGCAAGGCCCAATTCTACTTTTCCCATTGATAAATCCATGACTGTAGTTCTAACTTTTA
TAACTCCCATGCTGAACCCACTAATCTATACCCTGAAGAATGCAGAAATGAAAAGTGCCAT
30 GAGGAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA
(SEQ ID NO: 348)

AOLFR189 sequences:

MQQNSVPEFILLGLTQDPLRQKIVFVIFLIFYMGTVVGNMLIIVTIKSSRTLGSPPMYFFLFYLSF
35 ADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFALHLFGCMEIFVLILMAVDRYVAICKPLRYP
TIMSQQVCHILIVLAWIGSLIHSTAQIILALRLPFCGPYLIDHYCCDLQPLLKLACMDTYMINLLL
VNSGAICSSSFMIISIYVILHSLRNHSAKGKKKALSACTSHIIVVILFFGPCIFYTRPPTTFPMD
KMAVAFYITIGTFLNPLIYTSEECRSEKCHEK (SEQ ID NO: 349)

40 ATGCAGCAAAATAACAGTGTGCCTGAATTCATACTGTTAGGATTAACACAGGATCCCTTGA
GGCAGAAAATAGTGTTTGTAACTCTTCTTAATTTCTATATGGGAACTGTGGTGGGGAATAT
GCTCATTATTGTGACCATCAAGTCCAGCCGACACTAGGAAGCCCCATGTACTTCTTTCTA
TTTTATTTGTCCTTTGCAGATTCTTGCTTTTCAACTTCCACAGCCCCTAGATTAATTGTGGA
TGCTCTCTCTGAAAAGAAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTTGCACTA
45 CATTTATTTGGCTGCATGGAGATCTTTGTCCTCATTCTCATGGCTGTTGATCGCTATGTGGC
CATCTGTAAGCCCTTGCGTTACCCAACCATCATGAGCCAGCAGGTCTGCATCATCCTGATT
GTTCTTGCTTGATAGGGTCTTTAATACTCTACAGCTCAGATTATCCTGGCCTTAAGATT
GCCTTTCTGTGGACCCTATTTGATTGATCATTATTGCTGTGATTGTCAGCCCTTGTTGAAAC
TTGCCTGCATGGACACTTACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTTG
50 CTCAAGTAGTTTCATGATTTTGATAATTTTCATATATTGTCATCTTGCAATCACTGAGAAACC
ACAGTGCCAAAGGGAAGAAAAAGGCTCTCTCCGCTTGACGCTCTCACATAATTGTAGTCAT
CTTATCTTTGGCCCATGTATATTTCATATACACGCCCCCGACCACTTTCCCATGGACA
AGATGGTGGCAGATTTTATACTATTGGAACACCCCTTTCTCAATCCACTCATCTACACATCT
GAGGAATGCAGAAAGTAAAAAATGCCATGAGAAAG (SEQ ID NO: 350)

55

AOLFR190 sequences:

MQRSNHTVTEFILLGFTTDPGMQLGLFVVFLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN
LSFLDLWYSSVHTPKILVTCISEDKSISFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL
YAQTMPRRLCICLVLYSYTGGFVNAILTSNTFTLDFCGDNVIDDFCDVPPLVKLACSVRESYQ
5 AVLHFLLASNVISPTVLILASYLSIITILRIHSTQGRIKVFSTCSSHLISVTLYYGSIYNYSRPS
YSLKRDKMVSTFYTMLFPM LNPMIYSLRSKDMKDALKKFFKSA (SEQ ID NO: 351)

ATGCAGAGGAGCAATCACACAGTGACTGAGTTCATCCTGCTGGGCTTCACCACAGATCCAG
GGATGCAACTGGGCCTCTTTGTGGTGTTCTGGGTGTGTACTGTCTGACTGTGGTAGGAAG
10 TAGCACCTCATCGTGTTGATCTGTAATGACTCCCGCTACACACACCCATGTATTTGTCA
TTGGAAATCTGTCATTTCTGGATCTCTGGTATTCTTCTGTCCACACCCCAAAGATCCTAGTG
ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCAGTTCTTCTCTGC
CAGGCTGGCCTATAGTGAGTGCTACCTACTGGCTGCCATGGCTTATGACCACTACGTGGCC
ATCTCCAAGCCCCTGCTTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTTGGTTTT
15 ATATTCCTATACTGGGGGTTTTGTCAATGCAATAATATTAACCAGCAACACATTACATTG
GATTTTTGTGGTGACAATGTCATTGATGACTTTTTCTGTGATGTTCCACCCCTCGTGAAGCT
GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCCTTCTGGCCTCCAATGTC
ATCTCCCCTACTGTGCTCATCCTTGCTCTTACCTCTCCATCATCACCACCATCCTGAGGAT
CCTCTTACCCAGGGCCGCATCAAAGTCTTCTCCACATGCTCCTCCCACCTGATCTCCGTTA
20 CCTTATACTATGGCTCCATTCTCTACAACACTACTCCCGGCCAAGTTCAGCTACTCCCTCAAG
AGGGACAAAATGGTTTCTACCTTTTATACTATGCTGTTCCCATGTTGAATCCCATGATCTA
CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATTCTTCAAGTCAGCATAA
(SEQ ID NO: 352)

AOLFR191 sequences:

MTGGGNITEITYFILLGFSDFPRIKVLFTIFLVIYITSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS
FIDVCYISSTVPKMLSNLLQEQTTITFVGCIQYFIFSTMGLESCLMTAMAYDRYAICNPLLYS
SIMSPTLCVWMVLGAYMTGLTASLFQIGALLQLHFCGSNVIRHFFCDMPQLLLSCTDTFFVQV
5 MTAILTMFFGIASALVIMISYGYIGISIMKITSAGSPKAFNTCASHLTAVSLFYTSGIFVYLRSSS
GGSSSFDRFASVFYTVVIPMLNPLIYSLRNKEIKDALKRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTTCATCCTGCTGGGATTCTCAGATT
TTCCCAGGATCATAAAAGTGCTCTTCACTATATTCCTGGTGATCTACATTACATCTCTGGCC
10 TGGAACCTCTCCCTCATTGTTTAAATAAGGATGGATTCCCACCTCCATACACCCATGTATTT
CTTCCTCAGTAACCTGTCCTTCATAGATGTCTGCTATATCAGCTCCACAGTCCCCAAGATGC
TCTCCAACCTCTTACAGGAACAGCAAATATCACTTTTGTGGTTGTATTATTCAGTACTTT
ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT
ATGCTGCCATTTGTAACCCCTGCTCTATTCATCCATCATGTACCCACCCTCTGTGTTTG
15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATTCCAAATTGGTGCTTTGCT
TCAACTCCACTTCTGTGGGTCTAATGTCATCAGACATTTCTTCTGTGACATGCCCCAACTGT
TAATCTTGCTGTACTGACACTTTCTTTGTACAGGTCATGACTGCTATATTAACCATGTTT
TTTGGGATAGCAAGTGCCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA
TGAAGATCACTTCAGCTAAAGGCAGTCCAAAGGCATTCAACACCTGTGCTTCTCATCTAAC
20 AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTTGAGGTCCAGCTCTGGAGGTT
CTTCAAGCTTTGACAGATTTGCATCTGTTTTCTACACTGTGGTCATTCCCATGTTAAATCCC
TTGATTTACAGTTTGAGGAACAAAGAAATTAAAGATGCCTTAAAGAGGTTGCAAAAGAGA
AAGTGCTGCTGA (SEQ ID NO: 354)

AOLFR192 sequences:

MENNTEVTEFIVLGLTDDPELQIPLFIVFLFIYLIJTLVGNLGMIELILLDSCLHTPMYFFLSNLSLV
DFGYSSAVTPKVMVGF LTGDKFILYNACATQFFFFVAFITAESFLLASMA YDRYAALCKPLHY
TTTMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFCRSNVVEHFFCDAPPLTLSCSDNYISEM
VIFFVVGFNDFLSILVILISYLFIFITIMKMRSPEGRQKAFSTCASHLTAVSIFYGTGIFMYLRPNSS
30 HFMGTDKMASVFYAIVIPMLNPLVYSLRNKEVKSFAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTGGGGTTAACTGATGACCCAGAA
CTGCAGATCCCCTCTTCATAGTCTTCTTTTCATCTACCTCATCACTCTGGTTGGGAACCT
GGGGATGATTGAATTGATTCTACTGGACTCCTGTCTCCACACCCCATGTACTTCTTCTCA
35 GTAACCTCTCCCTGGTGGACTTTGGTTATTCTCAGCTGTCACTCCCAAGGTGATGGTGGG
GTTTCTCACAGGAGACAAATTCATATTATATAATGCTTGTGCCACACAATTCTTCTTTG
TAGCCTTTATCACTGCAGAAAGTTTCTCCTGGCATCAATGGCCTATGACCGCTATGCAGC
ATTGTGTAAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTTGCTGGCC
ATAGGCTCCTACATCTGTGGTTTCTGAATGCATCCATTCTACTGGGAACACTTTCAGGC
40 TCTCCTTCTGTAGATCCAATGTAGTTGAACACTTTTCTGTGATGCTCCTCCTCTCTTGACT
CTCTCATGTTTCAGACAACTACATCAGTGAGATGGTTATTTTTTTTGTGGTGGGATTCAATG
ACCTCTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTTATATTTATCACCATCATGAAG
ATGCGCTCACCTGAAGGACGCCAGAAGGCCTTTTCTACTTGTGCTTCCACCTTACTGCAG
TTTCCATCTTTTATGGGACAGGAATCTTTATGTACTTACGACCTAACTCCAGCCATTTTCATG
45 GGCACAGACAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG
TCTACAGCCTGAGGAACAAAGAGGTTAAGAGTGCCTTTAAAAGACTGTAGGGAAGGCAA
AGGCCTCTATAGGATTCATATTTTAA (SEQ ID NO: 356)

AOLFR193 sequences:

MENKTEVTQFILLGLTNDSELQVPLFITPFIYIITLVGNLGIIVLIFWDSCLHNP MYFFLSNLSLV
DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLLASMA YDRYA AVCKPLHY
TTTMTTTVCARLAIGSYLCGFLNASIHTGDTFSLSFCCKSNEVHFFCDIPAVMVLSCSDRHISEL
VLIYVVVSNIFIALLVILISYTFIFITILKMHSASVYQKPLSTCASHFIAVGIFYGTIIFMYLQPSSSH
SMDTDKMAPVFYTMVIPMLNPLVYSLRNKEVKSFAKKVVEKAKLSVGWSV (SEQ ID NO:
55 357)

ATGGAAAATAAGACAGAAGTAACACAATTCATTCTTCTAGGACTAACCAATGACTCAGAA
 CTGCAGGTTCCCTCTTTATAACGTTCCCTTCATCTATATTACTCTGGTTGGAAACCT
 GGGAATTATTGTATTGATATTCTGGGATTCTGTCTCCACAATCCCATGTACTTTTTTCTCA
 5 GTAACCTTGTCTCTAGTGGAAGTTTGTCTCTTCTCAGCTGTCACTCCCATCGTCATGGCTGGA
 TTCCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAATGTATATCTTTGT
 AGCTTTTGCCACTGTGGAAAATTACCTCTTGGCCTCAATGGCCTATGACCGCTATGCAGCA
 GTGTGCAAACCCCTACATTACACCACAACCATGACAACAACCTGTGTGTGCTCGTCTGGCCA
 TAGGCTCCTACCTCTGTGGTTTCTGAATGCCTCCATCCACACTGGGGACACATTTAGTCTC
 10 TCTTTCTGTAAGTCCAATGAAGTCCATCACTTTTTCTGTGATATTCCAGCAGTCATGGTTCT
 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTCTTATTTATGTTGTGAGCTTCAATATCT
 TTATAGCTCTCCTGGTTATCTTGATATCTACACATTCATTTTTATCACCATCCTAAAGATG
 CACTCAGCTTCAGTATACCAGAAGCCTTTGTCCACCTGTGCCTCTCATTTTCATTGCAGTCGG
 CATCTTCTATGGGACTATTATCTTCATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA
 CAGACAAAATGGCACCTGTGTTCTATACAATGGTCATCCCCATGCTGAACCCTCTGGTCTA
 15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT
 GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

AOLFR194 sequences:

MERQNSQSCVVEFILLGFSNYPELQGQLFVAFVLVIYLVTLIGNAIIIVIVSLDQSLHVPMYLFLNL
 20 SVVDLSFSASVIMPEMLVVLSTKTTISFGGCFQMYFILLFGGAECFLLGAMAYDRFAAICHPL
 NYQMIMNKGVMFKLIIFSWALGFMLGTQVTSWVSSFPFCGLNEINHISCETPAVLELACADFL
 FEIYAFTGTFLILVPLLLLSYIRVLFAILKMPSTTGRQKAFSTCAAHLTSTVLFYGTASMTYLO
 PKSGYSPETKKVMSLSYLLTPLLNLIIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO:
 359)

ATGGAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC
 CTGAGCTCCAGGGGAGCTCTTTGTGGCTTTCTGGTTATTTATCTGGTGACCTGATAGG
 AAATGCCATTATTATAGTCATCGTCTCCCTAGACCAGAGCCTCCACGTTCCCATGTACCTGT
 25 TTCTCCTGAACTTATCTGTGGTGGACCTGAGTTTCAGTGCAGTTATTATGCCTGAAATGCT
 GGTGGTCCCTCTCTACTGAAAAAACTACAATTTCTTTTGGGGGCTGTTTTGCACAGATGTAT
 30 TTCATCCTCTTTTTGGTGGGGCTGAATGTTTTCTTCTGGGAGCAATGGCTTATGACCGATT
 TGCTGCAATTTGCCATCCTCTCAACTACCAAATGATTATGAATAAAGGAGTTTTTATGAAA
 TTAATTATATTTTCATGGGCCTTAGGTTTTATGTTAGGTACTGTTCAAACATCATGGGTATC
 TAGTTTTCCCTTTTGTGGCCTTAATGAAATTAACCATATATCTTGTGAAACCCAGCAGTGT
 35 TAGAAGTTGCATGTGCAGACACGTTTTTGTGTTGAAATCTATGCATTACAGGCACCTTTTG
 ATTATTTTGGTTCCTTTCTTGTGATACTCTTGTCTTACATTTCGAGTTCTGTTTGCCATCCTG
 AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCGCTCACCTCACAT
 CTGTGACCCTATTCTATGGCACAGCCAGTATGACTTATTTACAACCCAAATCTGGCTACTC
 ACCGGAAACCAAGAAAGTGATGTCTTACTCACTTCTGACACCACTGCTGAATCTG
 40 CTTATCTACAGTTTGCAGAAATAGTGAGATGAAGAGGGCTTTGATGAAATTATGGCGAAGG
 CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

AOLFR195 sequences:

MIVQLICTVCFILAVNTFHVRSFDFLKADDMGEINQTLVSEFLLGLSGYPKIEIVYFALILVMY
 45 LVILIGNVLIASIFDSHFHTPMYFFLGNLSFLDICYTSSSVSTLVSLSKKRNISFSGCAVQMFF
 GFAMGSTECLLGMMAFDYVAICNPLRYPIILSKVAYVLMASVSWLSGGINSVQTLAMRL
 PFCGNNIINHFACEILAVKLACADISLNIITMVISNMAFLVPLMVIFFSYMFIYITLQMNSATG
 RRKAFSTCSAHLTVVIIFYGTIFFMYAKPKSQDLIGEEKLQALDKLISLFYGVVTPMLNPILYSRL
 NKDVKAARKYLLNKKPIH (SEQ ID NO: 361)

ATGATTGTTTCAGTTAATTTGTACTGTTTGTCTTGGCAGTAAATACATTTTCATGTTAGATC
 TTCTTTTGATTTCCTGAAAGCAGATGACATGGGTGAGATTAACCAGACACTTGTGTGAGAA
 TTTCTTCTTCTGGGTCTTTCTGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATTCT
 AGTTATGTACCTAGTGATTCTAATTGGCAATGGTGTCTAATCATAGCCAGCATCTTTGATT
 55 CTCATTTTCACACACCAATGTACTTCTTCTGGGCAACCTCTCTTTCTGGATATCTGCTAT
 ACATCCTCCTCTGTTCCCTCAACATTGGTGAGCTTAATCTCAAAGAAAAGAAACATTTCT

TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGAATGGGGTCAACAGAATGTCTGCT
TCTTGGCATGATGGCATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC
ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTTCTGTGTCCTGGCTGTCCGGTGAATAA
ATTCAGCTGTGCAAACTACTTGGCCATGAGACTGCCTTTCTGTGGGAATAATATTATCAA
5 TCATTTTCGCATGTGAAATATTAGCTGTCTCAAGCTGGCCTGTGCTGATATATCCCTCAATA
TTATCACCATGGTGATATCAAATATGGCCTTCTGCTTCTTCCACTGATGGTCATTTTTTTC
TCCTATATGTTTCATCCTCTACACCATCTTGCAAATGAATTCAGCCACAGGAAGACGCAAGG
CATTTTCCACGTGCTCAGCTCACCTGACTGTGGTGATCATATTTTACGGTACCATCTTCTTT
ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAATTGCAAGCATTAGAC
10 AAGCTCATTTCTCTGTTTTATGGGGTAGTGACCCCATGCTGAATCCTATACTCTATAGCTT
GAGAAATAAGGATGTAAAAGCTGCTGTAAAATATTTGCTGAACAAAAAACCAATCACTA
A (SEQ ID NO: 362)

AOLFR196 sequences:

15 MLESNYTMPTEFLVGFDTDYPLRVTLFLVLLVYTLTMVGNILLIILVNINSSLQIPMYFSLN
SFLDISCSTAITPKMLANFLASRKSSISPYGCALQMFFFAFADAECLILAAMAYDRYAAICNPLL
YTTLMSSRRVCVCFIVLAYFSGSTSLVHVCLTFRLSFCGSNIVNHFFCDIPLLALSCTDQTQINQL
LLFALCSFIQTSTFVVIFISYFCILITVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS
YSLDTDKVAVFYTVVFPMPFNPIIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ
20 ID NO: 363)

ATGTTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTTGTTGGATTACAGATTATC
TACCTCTCAGAGTCACACTGTTCTTGGTATTCCTTCTGGTATATACATTAAGTATGGTCGGA
AATATACTCTTAATAATTCTAGTTAATATTAATTCAAGCCTTCAAATTCCTCATGTATTATTT
25 TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTTCTACAGCAATCACTCCTAAAATGCTGG
CAAACCTCTTGGCATCCAGGAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTTT
CTTCGCTTCTTTTGTGCTGATGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGACCGCTATG
CAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGTCTGTGTCTGCTT
CATTGTGTTGGCATATTTTCACTGGAAGTACAACATCACTGGTCCATGTGTGCCTCACATTC
30 AGGCTGTCATTTTGTGGCTCCAATATCGTCAATCATTTTTTCTGTGATATCCCACCTCTTCT
GGCTTTATCATGTACAGACACTCAGATCAACCAGCTTCTGCTCTTTGCTTTGTGCAGCTTCA
TCCAGACCAGCACTTTTGTGGTAATATTTATTTCTTACTTCTGCATCCTCATCACTGTGTTG
AGCATCAAGTCCTCAGGTGGCAGAAGCAAAACATTCTCCACTTGTGCTTCCCACCTCATAG
CAGTCACCTTATTCTATGGAGCGCTCTGTTTATGTACTTACAGCCCACCACTAGCTATTCC
35 CTAGACACTGATAAGGTGGTGGCAGTGTTTATACTGTTGTATTTCCTATGTTTAATCCAA
TAATTTATAGTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA
TTGGATATTCAAATGAATGGTATTTAAATCGTTTAAAGATAGTCAATATCTAA (SEQ ID NO:
364)

AOLFR197 sequences:

40 MCYLSQLCLSLGEHTLHMGVMVRHTNESNLAGFILLGFSDYPQLQKVLFLVILILYLLTILGNTTI
ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNHALGS
TECVLLALMSCDRYVAVCRPLHYTVLMHIHLMLALASMAWLSGIATTLVQSTLTLQLPFCGH
RQVDHFICEVPVLIKACVGTTFNEAELFVASILFLIVPVSFILVSSGYIAHAVLRIKSATRRQKAF
45 GTCFSLHTVVTIFYGTIIFMYLQPAKSRSDQGKFVSLFYTVVTRMLNPLIYTLRIKEVKGALKK
VLAKALGVNIL (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG
TGAGACATACCAATGAGAGCAACCTAGCAGGTTTCATCCTTTTAGGGTTTCTGATTATCC
50 TCAGTTACAGAAGGTTCTATTTGTGCTCATATTGATTCTGTATTTACTAACTATTTTGGGGA
ATACCACCATCATTCTGGTTTCTCGTCTGGAACCCAAGCTTCATATGCCGATGTATTTCTTC
CTTTCTCATCTCTCCTTCTGTACCGCTGCTTACCAGCAGTGTTATTTCCCAGCTCCTGGT
AAACCTGTGGGAACCCATGAAAACATATCGCCTATGGTGGCTGTTTGGTTACCTTTACAAC
TCCCATGCCCTGGGATCCACTGAGTGCGTCTCTTGGCTCTGATGTCCTGTGACCGCTATGT
55 GGCTGTCTGCCGTCTCTCCATTACACTGTCTTAATGCATATCCATCTCTGCATGGCCTTGG
CATCTATGGCATGGCTCAGTGGAATAGCCACCACCCTGGTACAGTCCACCCTCACCTGCA

GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTTCATCTGCGAGGTCCCTGTGCTCATC
AAGCTGGCTTGTGTGGGCACACGTTTAACGAGGCTGAGCTTTTTGTGGCTAGTATCCTTT
TCCCTATAGTGCCTGTCTCATTATCCTGGTCTCCTCTGGCTACATTGCCCACGCAGTGTG
5 AGGATTAAGTCAGCTACCAGGAGACAGAAAGCATTGGGACCTGCTTCTCCACCTGACA
GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT
CCAGGGACAGGGCAAGTTTGTCTCTCTTCTACACTGTGGTAACCCGCATGCTTAACCC
TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAA
GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)

10 **AOLFR198 sequences:**

MENCTEVTKFILLGLTSVPELQIPLFILFTFIYLLTLCGNLGMMLLILMDSCLHTPMYFFLSNLSL
VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFFVALATVENYLLASMA YDRYA AVCKP
LHYTTTMTASVGACLALGSYVCGFLNASFHIGGIFSLSFCKSNLVHHFFCDVPAVMALSCSDKH
TSEVILVFMSSFNIFVLLVIFISYLFIFITILKMHSAGKHQKALSTCASHFTAVSVFYGTVIFIYLO
15 PSSSHMDTDKMASVFIAMHPLNPVVYSLRNREVQNAFKKVLRRQKFL (SEQ ID NO: 367)

ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCCAGAAC
TACAGATCCCCCTCTTTATCTTGTTCACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG
20 GGGATGATGTTGCTGATCCTGATGGACTCTTGTCTCCACACCCCATGTACTTTTTCTCAG
TAACCTGTCTCTGGTGGACTTTGGATACTCCTCAGCTGTCACTCCCAAGGTCATGGCTGGG
TTCCTTAGAGGAGACAAGGTCATCTCCTACAATGCATGTGCTGTTTCTTCTTTGT
AGCCTTGGCCACGGTGGAAAATTACTTGTGGCCTCAATGGCCTATGACCGCTATGCAGCA
GTGTGCAAACCCCTACACTACACCACCACCATGACGGCCAGTGTAGGTGCCTGTCTGGCCC
TAGGCTCATATGTCTGTGGCTTCCTAAATGCCTCATTCCACATTGGGGGCATATTCAGTCTC
25 TCTTTCTGTAAATCCAATCTGGTACATCACTTTTCTGTGATGTTCCAGCAGTCATGGCTCT
TCTTGTCTCTGATAAACACACTAGTGAGGTGATTCTGGTTTTTATGTCAAGCTTTAATATCT
TTTTTGTCTTCTAGTTATCTTTATCTCCTACTTGTTTCATATTCATCACCATCTTGAAGATGC
ATTCAGCTAAGGGACACCAAAAAGCATTGTCCACCTGTGCCTCTCACTTCACTGCAGTCTC
CGTCTTCTATGGGACAGTAATCTTCATCTACTTGCAGCCCAGCTCCAGCCACTCCATGGAC
30 ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCCATGCTGAACCTGTGGTCT
ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTGAGAAGGCAAAAAT
TTCTATAA (SEQ ID NO: 368)

35 **AOLFR199 sequences:**

MDTGNTLTPQDFLLLGFPQSQTQLQSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS
NLSFLEIWIYTTAAVPKALAILLGRSQTISFTSCLLQMYFVFSLGCTEYFLLAAMAYDRCLAICY
LHYGAIMSSLLSAQLALGSWVCGFVAIAVPTALISGLSFCGPRAINHHFFCDIAPWIALACTNTQA
VELVAFVIAVVVILSSCLITFVSYYIISTILRIPSASGRSKAFSTCSSHLTVVLIWYGSTVFLHVR
TSIKDALDLIAVHVLNTVTVLPVLPFIYTLRNKEVRETLKKWKWK (SEQ ID NO: 369)

40 ATGGACACAGGCAACAAAACCTCTGCCCCAGGACTTTCTCTTACTGGGCTTTCTGGTTCTC
AAACTCTTCAGCTCTCTCTCTTTATGCTTTTTCTGGTGATGTACATCCTCACAGTTAGTGGT
AATGTGGCTATCTTGATGTTGGTGAGCACCTCCCATCAGTTGCATACCCCATGTACTTCTT
TCTGAGCAACCTCTCCTTCCTGGAGATTGGTATACCACAGCAGCAGTGCCCAAAGCACTG
45 GCCATCCTACTGGGGAGAAGTCAGACCATATCATTACAAAGCTGTCTTTGCAGATGTACT
TTGTTTTCTCATTAGGCTGCACAGAGTACTTCCTCCTGGCAGCCATGGCTTATGACCGCTGT
CTTGCCATCTGCTATCCTTTACACTACGGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC
TGGCCCTGGGCTCCTGGGTGTGTGGTTTCGTGGCCATTGCAGTGCCACAGCCCTCATCAG
TGGCCTGTCTTCTGTGGCCCCCGTGCCATCAACCACTTCTTCTGTGACATTGCACCCTGGA
50 TTGCCCTGGCCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATTGCTGTTGT
GGTTATCCTGAGTTTCATGCCTCATCACTTTGTCTCCTATGTGTACATCATCAGCACCATCC
TCAGGATCCCCTCTGCCAGTGGCCGGAGCAAAGCCTTCTCCACGTGCTCCTCGCATCTCAC
CGTGGTGCTCATTGTTATGGGTCCACAGTTTTCTTTCACGTCCGCACCTCTATCAAAGAT
GCCTTGGATCTGATCAAAGCTGTCCACGTCTGAACACTGTGGTGACTCCAGTTTAAACC
55 CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG
GAAAATAA (SEQ ID NO: 370)

AOLFR200 sequences:

MTRKNYTSLTEFVLLGLADTLELQIILFLFFLVYITLTVLGNLGMILLIRIDSQ LHTPMYFFLANL
SFVDVCNSTTITPKMLADLLSEKKTISFAGCFLQMYFFISLATTECILFGLMAYDRYAAICRPLL
5 YSLIMSRTVYLKMAAGAFAGLLNFMVNTSHVSSLSFCDSNVIIHFFCDSPLFLKSCSDTILKE
SISSILAGVNIVGTLLVILSSYSYVLFISFMSHSGEGRHRAFSTCASHLTAILFYATCIYTYLRPSS
SYSLNQDKVASVFTVVIPMLNPLIYSLRSKEVKKALANVISRKRTSSFL (SEQ ID NO: 371)

ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGC
10 TGGAGCTACAGATTATCCTCTTTTTGTTTTTCTTGATTTATACACTTACAGTACTGGGA
AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCCAGCTTCACACACCCATGTATTTCTT
CCTGGCTAACCTGTCCTTTGTGGACGTTTGTAACCTCACTACCATCACCCCAAAGATGCTG
GCAGATTTATTATCAGAGAAGAAAACCATCTCTTTGCTGGCTGCTTCCTACAGATGTACT
TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTAAATGGCCTATGACAGGTA
15 TGCGGCCATATGTCGCCCCGCTGCTTTACTCCTTGATCATGTCCAGGACCGTCTACCTAAAA
ATGGCAGCCGGGGCTTTGCTGCAGGGTGTGCTGAACCTTCATGGTCAACACAAGCCATGTCA
GCAGCTTGTCATTCTGTGACTCCAATGTCATCCATCACTTCTTCTGTGACAGTCCCCCACTT
TTCAAGCTCTCTTGTTCTGACACAATCCTGAAAGAAAGCATAAGTTCTATTTTGGCTGGTG
TGAATATTGTGGGGACTCTGCTTGTATCCTCTCCTCCTACTCCTACGTTCTCTTCTCCATT
20 TTTTCTATGCATTCGGGGGAGGGGAGGCACAGAGCTTTCTCCACGTGTGCCTCTCACCTGA
CAGCCATAATTCTGTTCTATGCCACCTGCATCTATACTTACCTGAGACCTAGTTCCAGTAC
TCCCTGAATCAGGACAAAGTGGCTTCTGTGTTCTACACAGTGGTGATTCCCATTGTGAATC
CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAGGCTTTAGCGAATGTAATTAGCA
GGAAAAGGACCTCTTCCTTTCTGTGA (SEQ ID NO: 372)

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AOLFR201 sequences:

MEWENHTILVEFFLKGLSGHPRELLFFVLIFIMYVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTTSIPSTLVSFLSERKTISLSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
YPIIMSKDAYVPMAAGSWIIGAVNSAVQSVFVQLPFCRNNIINHFTCEILAVMKLACADISDN
30 EFIMLVATTLFILTPLLLIIVSYTLIIVSIFKISSSEGRSKASSTCSAHLTVVIIFYGTILFMYMKPKS
KETLNSDDL DATDKIISM FYGVMT PMNPLIYSLRNKDVKEAVKHLLNRRFFSK (SEQ ID NO:
373)

ATGGAATGGGAAAACACACCACTTCTGGTGGAATTTTTCTGAAGGGACTTTCTGGTCACC
35 CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCACTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG
TGAGCTTCCTTTCAGAAAAGAAAGACCATTTCCTTTCTGGCTGTGCAGTGCAGATGTTCTT
CGGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT
40 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCTGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTGTTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTGGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT
TGTTTCATATTGACACCTTTGTTATTAATCATTTGTCTCTTACACGTTAATCATTGTGAGCATC
45 TTCAAAATTAGCTCTTCCGAGGGGAGAAGCAAAGCTTCTCTACCTGTTACGCCCATCTGA
CTGTGGTCATAATATTCTATGGGACCATCCTCTTCATGTACATGAAGCCCAAGTCTAAAGA
GACACTTAATTCGGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGTAAGAGGCA
GTAAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

50

AOLFR202 sequences:

MEWENHTILVEFFLKGLSGHPRELLFFVLIFIMYVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTTSIPSTLVSFLSERKTISLSGCAVQMFLSLAMGTTECVLLGVMAFDRYVAICNPLR
YPIIMSKDAYVPMAAGSWIIGAVNSAVQTVFVQLPFCRNNIINHFTCEILAVMKLACADISGN
55 EFILLVTTLFLLTPLLLIIVSYTLIISIFKISSSEGRSKPSSTCSARLTVVITFCGTIFLMYMKPKSQ

ETLNSDDLDATDKLIFIFYRVMTPMMNPLIYSLRNKDVKEAVKHLLRRKNFNK (SEQ ID NO: 375)

5 ATGGAATGGGAAAACACACCATTCTGGTGGAAATTTTTCTGAAGGGACTTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG
TGAGCTTCCTTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCT
10 CAGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCGTGATGGCCTTTGACCGCTAT
GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCTTGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTTTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTAGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGGCAATGAGTTCATCCTGCTTGTGACCACAACAT
15 TGTTCTATTGACACCTTTGTTATTAATTATTGTCTCTTACACGTTAATCATTTTGAGCATC
TTCAAATTAGCTCTTTCGGAGGGGAGAAGCAACCTTCTCTACCTGCTCAGCTCGTCTGA
CTGTGGTGATAACATTCTGTGGGACCATCTTCCCTCATGTACATGAAGCCCAAGTCTCAAGA
GACACTTAATTGAGTACTGACTGGATGCCACTGACAACTTATATTTCATATTCTACAGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA
20 GTAAACACCTACTGAGAAGAAAAAATTTTAACAAGTAA (SEQ ID NO: 376)

AOLFR203 sequences:

MKRQNQSCVVEFILLGFSNFPQLVQLFGVFLVIYVVTLMGNAIITVIISLNQSLHVPMYLFLN
LSVVEVSFSVITPEMLVVLSTKTMISFVGCFAQMYFILLFGGTECFLLGAMAYDRFAAICHPL
25 NYPVIMNRGVFMKLVIFSWISGIMVATVQTTWVFSFPFCGPNEINHLCETPPVLELVCADTFLF
EIYFTGTLIVMVPFLILLISYIRVLFALKMPSTTGRQKAFSTCASHLTSVTLFYGTANMTYLO
PKSGYSPETKKLISLAYTLLTPLLNPLIYSLRNSEMKRTLIKLWRRKVILHTF (SEQ ID NO: 377)

30 ATGAAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCCTGGGCTTTTCTAACTTTC
CTGAGCTCCAGGTGCAGCTCTTTGGGGTTTTCTAGTTATTTATGTGGTGACCCTGATGGG
AAATGCCATCATTACAGTCATCATCTCCTTAAACCAGAGCCTCCACGTTCCCATGTACCTGT
TCCTCCTGAACCTATCTGTGGTGGAGGTGAGTTTCACTGCAGTCATTACGCCTGAAATGCT
GGTGGTGCTCTCTACTGAGAAAATATGATTTCTTTTGTGGGCTGTTTTGCACAGATGTAT
TTCATCCTTCTTTTTGGTGGGACTGAATGTTTTCTCCTGGGAGCGATGGCTTATGACCGATT
35 TGCTGCAATTTGCCATCCTCTGAACTACCCAGTGATTATGAACAGAGGGGTTTTATGAAA
TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGACCACTTGGGTAT
TTAGTTTTCCATTTTGTGGCCCCAATGAAATTAATCATCTCTTCTGTGAGACTCCCCCGGTA
CTAGAGCTTGTGTGTGCAGACACCTTCTTATTTGAAATCTATGCCTTCACAGGCACCATTTT
GATTGTTATGGTTCCTTTCTTGTGTGATCCTCTTGTCTTACATTTCGAGTTCTGTTGCCATCCT
40 GAAGATGCCATCAACTACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCTCTCACCTCACA
TCTGTGACCTGTTCTATGGCACAGCCAATATGACTTATTTACAACCCAAATCTGGCTACTC
ACCCGAAACCAAGAACTGATCTCATTGGCTTACACGTTGCTTACCCCTCTGCTCAATCCG
CTCATCTATAGCTTACGAAACAGTGAGATGAAGAGGACTTTGATAAACTATGGCGAAGA
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

AOLFR204 sequences:

45 MEKKKNVTEFILIGLTQNPIMEKVTFVFLVLYMITLSGNLLIVVTITTSQALSSPMYFFLTHLSL
IDTVYSSSSAPKLIVDSFQEKKIISFNGCMAQAYAEHIFGATEIILLTVMACDCYVAICKPLNYTT
IMSHSLCILLVAVAVWVGFLHATIQILFTVWLPFCGPNVIGHFMCDLYPLLKLVCIDHTLGLFV
AVNSGFICLLNFLILVVSYYIILRSLKNSLEGRCKALSTCISHIIVVLFVPCIFVYLRSVTTLP
50 DKAVAVFYTMVVPMLNPVYTLRNAEVKSAIRKLWRKKVTSND (SEQ ID NO: 379)

ATGGAGAAGAAAAAGAATGTGACTGAATTCATTTTAATAGGTCTTACACAGAACCCCAT
ATGGAGAAAGTCACGTTTGTAGTATTTTGGTTCTTTACATGATAACACTTTCAGGCAACC
TGCTCATTGTGGTTACCATTACCACCAGCCAGGCTCTGAGCTCCCCATGTACTTCTTCTCT
55 ACCCACCTTTCTTTGATAGACACAGTTTATTCTTCTTCTTCTCAGCTCCTAAGTTGATTGTGA
TTCCTTTCAAGAGAAGAAAATCATCTCCTTTAATGGGTGTATGGCTCAAGCCTATGCAGAA

CACATTTTTGGTGTCTACTGAGATCATCCTGCTGACAGTGATGGCCTGTGACTGCTATGTGG
CCATCTGCAAACCTCTGAACTACACAACCATATGAGCCACAGCCTGTGCATTCTCCTGGT
GGCAGTGGCCTGGGTGGGAGGATTTCTTCATGCAACTATTCAGATTCTCTTTACAGTATGG
CTGCCCTTCTGTGGCCCCAATGTCATAGGCCACTTCATGTGTGACTTGTACCCATTGTAAA
5 ACTTGTTTGCATAGACACTCATACCCTTGGTCTCTTTGTTGCTGTGAACAGTGGGTTTATCT
GCTTATTAAACTTCCTTATCTTGGTGGTATCCTATGTGATCATCTTGAGATCTTTAAAGAAC
AATAGCTTGGAGGGGAGGTGTAAAGCCCTCTCCACCTGTATTTCTCACATCATAGTAGTTG
TCTTATTCTTTGTGCCCTGTATATTTGTGTATCTGCGCTCAGTGACCACTCTGCCCATTGAT
AAAGCTGTTGCTGTATTTTATACTATGGTGGTCCCAATGTTAAATCCCGTGGTCTACACAC
10 TCAGAAATGCTGAGGTAAAAAGTGCAATAAGGAAGCTTTGGAGAAAAAAGTGAAGTTCAG
ATAATGATTAA (SEQ ID NO: 380)

AOLFR205 sequences:

MESENRTVIREFILLGLTQSQDIQLLVFVLVLIIFYFILPGNFLIIFTIKSDPGLTAPLYFFLGNLAFL
15 DASYSFTVAPRMLVDFLSAKKIISYRGCTQLFFLHFLGGGEGLLLVMMAFDRIYAICRPLHYPT
VMNPRTCYAMMLALWLGGFVHSHIQVVLRLPFCGPNQLDNFFCDVPQVIKLACTDTFVVEL
LMVFNSGLMTLLCFLGLASYAVILCRIRGSSSEAKNKAMSTCITHIIVIFFMFGPGIFIYTRPFRA
FPADKVVSLFHTVIFPLNPVIYTLRNQEVKASMKKVFKNHIA (SEQ ID NO: 381)

20 ATGGAAAGCGAGAACAGAACAGTGATAAGAGAATTCATCCTCCTTGGTCTGACCCAGTCT
CAAGATATTCAGCTCCTGGTCTTTGTGCTAGTTTTAATATTCTACTTCATCATCCTCCCTGG
AAATTTTCTCATTTATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCT
TTCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTCACTGTGGCTCCCCGGATGTG
GTGGACTTCTCTCTGCGAAGAAGATAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTT
25 TCTTGCACTTCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTA
CATCGCCATCTGCCGGCCTCTGCACTATCCTACTGTGCATGAACCCTAGAACCTGCTATGCA
ATGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCTCATCCT
CCGCTTGCCTTTTTGTGGCCCAAACCAGCTGGACAACTTCTTCTGTGATGTCCACAGGTC
ATCAAGCTGGCCTGCACCGACACATTTGTGGTGGAGCTTCTGATGGTCTTCAACAGTGGCC
30 TGATGACACTCCTGTGCTTTCTGGGGCTTCTGGCCTCCTATGCAGTCATTCTTTGTGCATA
CGAGGGTCTTCTTCTGAGGCAAAAAACAAGGCCATGTCCACGTGCATCACCCATATCATTG
TTATATTCTTCATGTTTGGACCTGGCATCTTCATCTACACGCGCCCCCTTACGGGCTTTCCCA
GCTGACAAGGTGGTTTCTCTCTTCCACACAGTGATTTTTCTTTGTTGAATCCTGTCAATTA
TACCCTTCGCAACCAGGAAGTGAAAGCTTCCATGAAAAAGGTGTTTAATAAGCACATAGC
35 CTGA (SEQ ID NO: 382)

AOLFR206 sequences:

MANRNNVTEFILLGLTENPKMQKIIFVVSVIYINAMIGNVLIVVTITASPSLRSPMYFFLAYLSFI
DACYSSVNTPKLITDSLYENKTILFNGCMTQVFGEHFFRGVEVILLTVMAYDHYVAICKPLHYT
40 TIMKQHVCSLLVGVSWVGFLHATIQLFICQLPFCGPNVIDHFMCDLYTLINLACTNTHTLGLF
IAANSFICLLNCLLLLVS CVVILYSLKTHSLEARHEALSTCVSHITVVILSFIPCFVYMRPPATL
PIDKAVAVFYTMITSMLNPLIYTLRNAQMKNAIRKLCSRKAISSVK (SEQ ID NO: 383)

ATGGCGAATAGAAACAATGTGACAGAGTTTATTCTATTGGGGCTTACAGAGAATCCAAAA
45 ATGCAGAAAATCATATTTGTTGTGTTTTCTGTCTATCTACATCAACGCCATGATAGGAAATG
TGCTCATTGTGGTCACCATCACTGCCAGCCCATCACTGAGATCCCCCATGTACTTTTTCCTG
GCCTATCTCTCCTTTATTGATGCCTGCTATTCTCTGTCAATACCCCTAAGCTGATCACAGA
TTCATCTATGAAAACAAGACTATCTTATTCAATGGATGTATGACTCAAGTCTTTGGAGAA
CATTTTTTCAGAGGTGTTGAGGTATCCTACTTACTGTAATGGCCTATGACCACTATGTGG
50 CCATCTGCAAGCCCTTGCACTATACCACCATCATGAAGCAGCATGTTTGTAGCCTGCTAGT
GGGAGTGTGATGGGTAGGAGGCTTTCTTCATGCAACCATAACAGATCCTCTTCATCTGTCAA
TTACCTTTCTGTGCTCCTAATGTCTATAGATCACTTTATGTGTGATCTCTACACTTTGATCAA
TCTTGCTGCACTAATACCCACACTCTAGGACTCTTCATTGCTGCCAACAGTGGGTTTCATAT
GCCTGTAAACTGTCTCTTGCTCCTGGTCTCCTGCGTGGTCATACTGTACTCCTTAAAGACC
55 CACAGCTTAGAGGCAAGGCATGAAGCCCTCTCTACCTGTGTCTCCACATCACAGTTGTCA
TCTTATCCTTTATACCCTGCATATTTGTGTACATGAGACCTCCAGCTACTTTACCCATTGAT

AAAGCAGTTGCTGTATTCTACACTATGATAACTTCTATGTTAAACCCCTTAATCTACACCTT
GAGGAATGCTCAAATGAAAAATGCCATTAGGAAATGTGTAGTAGGAAAGCTATTTCAAG
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIIFDSHLHTPMYFFLCN
LSFLDVCYTSSSVPLILASFLAVKKKVSFSGCMVQMFISFAMGATECMILGTMALDRYVAICYP
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFAAMQLPFCANNVIKHFVCEILAILKLACADI
SINVISM TGSNLIVLVIPLLVISISYIFIVATILRIPSTEGKHKAFSTCSAHLTVVIIFYGTIFFMYAKP
10 ESKASVDSGNEDIIEALISLFYGVMTPLNPLIYSLRNKDVKA AVKNILCRKNFSDGK (SEQ ID
NO: 385)

ATGGAAGGACCAACGATTCCACGTCGACAGAATTTTCTCGGTAGGGCTTTCTGCCCACC
CAAAGCTCCAGACAGTTTTCTTCGTTCTAATTTTGTGGATGTACCTGATGATCCTGCTTGGG
15 AATGGAGTCCTTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCATGTATTTCTT
CCTCTGTAATCTTTCCTTCCTCGACGTTTGCTACACAAGTTCCTCTGTCCCACTAATTTCTTG
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCTTCTCTGGGTGTATGGTGCAAATGTTTAT
TTCTTTTGCCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCTAT
GTGGCCATCTGCTACCCACTGAGATACCCTGTCATCATGAGCAAGGGTGCCTATGTGGCCA
20 TGGCAGCTGGGTCTGGGTCACTGGGCTTGTGGACTCAGTAGTGCAGACAGCTTTTGCAAT
GCAGTTACCATTCTGTGCTAATAATGTCATTAAACATTTTGTCTGTGAAATTCTGGCTATCT
TGAAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTATGACAGGGTCTGAATCTGAT
TGTTCTGGTTATTCCATTGTTAGTAATTTCCATCTCTTACATATTTATTGTTGCCACTATTCT
GAGGATTCCTTCCACTGAAGGAAAAACATAAGGCCTTCTCCACCTGCTCAGCCCACCTGACA
25 GTGGTGATTATATTCTATGGAACCATCTTCTTCATGTACGCAAAGCCTGAGTCTAAGCCCT
CTGTTGATTAGGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTTCTATGGAGTGAT
GACTCCCATGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAAGGCTGCTGTC
AAAAACATACTGTGTAGGAAAAACTTTTCTGATGGAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIIFAVCLLMYLLGNIFLISITILDSHLHTPMYFLSNL
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP
LRYPVIMNRRTCVCQIAAGSWMTGCLTAMVEMMSVLPPLSLCGNSIINHFTCEILAILKLVCVDT
LVQLIMLVISVLLLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFYGTALSMH
35 LKPSAVDSQEIDKFMALVYAGQTPMLNPIIYSLRNKEVKVALKLLIRNHFNTAFISILK (SEQ
ID NO: 387)

ATGTTCCCGGCAAATTGGACATCTGTAAAAGTATTTTCTTCCTGGGATTTTTCCTACTACCC
CAAAGTTCAGGTCATCATATTTGCGGTGTGCTTGCTGATGTACCTGATCACCTTGCTGGGC
40 AACATTTTCTGATCTCCATCACCATTCTAGATTCCCACCTGCACACCCCTATGTACCTCTT
CCTCAGCAATCTCTCTTTCTGGACATCTGGTACTCCTCTTCTGCCCTCTCTCCAATGCTGG
CAAATTTGTTTCAGGGAGAAACACTATTTTCAATCTCAGGGTGCGCCACTCAGATGTACCT
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCCATGATGGCATATGACCGGTAT
GTGGCCATCTGCAACCCCTGAGATACCCTGTCATCATGAATAGGAGAACCTGTGTGCAGA
45 TTGCAGCTGGCTCCTGGATGACAGGCTGTCTCACTGCCATGGTGGAATGATGTCTGTGCT
GCCACTGTCTCTGTGGTAATAGCATCATCAATCATTTCACTTGTGAAATTCTGGCCATCT
TGAAATTGGTTTGTGTGGACACCTCCCTGGTGCAGTTAATCATGCTGGTGATCAGTGTACT
TCTTCTCCCATGCCAATGCTACTCATTTGTATCTCTTATGCATTTATCCTCGCCAGTATCC
TGAGAACTCAGCTCAGTGAAGGTGCAAGTAAAGCCTTTTCAACGTGCACAGCCCACTGA
50 TGGTGGTAGTTTGTCTATGGGACGGCTCTCTCCATGCACCTGAAGCCCTCCGCTGTAGA
TTCACAGGAAATAGACAAATTTATGGCTTTGGTGTATGCCGGACAAACCCCATGTTGAAT
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATTGCTGATTA
GAAATCATTTTAATACTGCCTTCATTTCCATCCTCAAATAA (SEQ ID NO: 388)

AOLFR209 sequences:

MDKINQTFVREFILLGLSGYPKLEIIFLALILVMYVVLIGNVLIASILDSRLHMPMYFFLGNLS
 5 FLDICYTTSSIPSTLVSLISKRNISFSGCAVQMFFGFAMGSTECFLLGMMAFDRYVAICNPLRY
 PIIMNKVVYVLLTSVSWLSGGINSTVQTSLAMRWPF CGNNIINHFLCEILAVLKLACSDISVNIV
 TLAVSNIAFLVLP LLVIFFSYMFILYTLIRTN SATGRHKAFSTCSAHLTVVIIIFYGTIFFMYAKPKS
 QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:
 389)

10 ATGGACAAGATAAACCAGACATTTGTGAGAGAATTCATTCTTCTGGGACTCTCTGGTTACC
 CCAAACCTGAGATCATTTTCTTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC
 AATGGTGTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCCATGTACTTCTT
 CCTGGGCAACCTCTCTTTCTGGATATCTGCTATACAACCTCCTCCATTCCCTCAACACTGG
 TGAGCTTAATCTCAAAGAAAAGAAACATTTCTTCTCTGGATGTGCAGTGCAGATGTTCTT
 15 TGGGTTTGCAATGGGGTCAACAGAATGTTTCTTCTTGGCATGATGGCATTGTGATCGTTAT
 GTGGCCATCTGTAACCCCTCTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC
 TGACTTCTGTATCATGGCTTTCTGGTGGAAATCAATTCAACTGTGCAACATCACTTGCCAT
 GCGATGGCCTTTCTGTGGGAACAATATTATTAATCATTCTTATGCGAGATCTTAGCTGTCC
 TAAATAGCTTGTTCTGATATATCTGTCAATATTGTTACCCTAGCAGTGTCAAATATTGCT
 20 TTCCTAGTTCTTCTCTGCTCGTGATTTTTTCTCCTATATGTTTCATCCTCTACACCATCTTG
 CGAACGAACCTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG
 TGGTGATCATATTTTATGGTACCATCTTCTTTATGTATGCAAAACCTAAGTCCAGGACCTC
 CTTGGGAAAGACAACCTTGCAAGCTACAGAGGGGCTTGTTCATGTTTTATGGGGTTGTGA
 CCCCCATGTTAAACCCATAATCTATAGCTTGAGAAATAAAGATGTAAAAGCTGCTATAAA
 25 ATATTTGCTGAGCAGGAAAGCTATTAACCAGTAA (SEQ ID NO: 390)

AOLFR210 sequences:

MMGRNRDNTNVADFILTGLSDSEEVQMALFMLFLLIYLITMLGNVGMILLIIRLDLQLHTPMYFFL
 THLSFIDLSTVTPKTLANLLTSNYISFTGCF AQMFVFLGTAECYLLSSMAYDRYAAICSP
 30 LHYTVIMPKRLCLALITGPYVIGFMDSFVNVVSMRSLHFCD SNIIHHFFCDTSPILALSCTDTDN
 TEMLIFIIAGSTLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTFIFYGTMIFTYLPK
 RKSYSLGRDQVAPVFYTIVIPMLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)

35 ATGATGGGTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC
 TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTTCTCCTCATATACCTAATTACTATGCT
 GGGGAATGTGGGGATGCTATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTAT
 TTTTCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAAC
 CTTAGCGAACTTACTGACTTCCAACATAATTTCTTACGGGCTGCTTTGCCAGATGTTCT
 GTTTGTCTTCTTGGGTACTGCTGAATGTTATCTTCTCTCCTCAATGGCCTATGATCGCTAT
 40 GCAGCGATCTGCAGTCTCTACACTACACAGTTATTATGCCCAAAGGCTCTGCCTCGCTC
 TCATCACTGGGCCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC
 AGATTGCATTTCTGTGACTCAAACATAATTCATCACTTTTCTGTGACTTCCCCAATTTT
 AGCTCTGTCTGCACTGACACAGACAACACTGAAATGCTGATATTCATTATCGCTGGTTCC
 ACCCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCT
 45 GAAAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCGTCTCTCATCTCTTG
 GGAGTCACCATCTTCTATGGAACATGATTTTTACTTACTTAAAGCCAAGAAAGTCTTATT
 CCTTGGGAAGAGATCAAGTGGCTCCTGTGTTTTATACTATTGTGATTCCCATGCTGAATCC
 ACTCATTTATAGTCTTAGAAACAGAGAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG
 AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)

AOLFR211 sequences:

MMGRNRNNTNVADFILMGLTLSEEIQMALFMLFLLIYLITMLGNVGMILLIIRLDLQLHTPMYFFL
 THLSFIDLSTVTPKTLANLLTSNYISFTGCF AQMFFFAFLGTAECYLLSSMAHDRYAAICSP
 LHYTVIMSKRLCLALITGPYVIGFIDSFVNVVSMRSLHFYDSNVIHHFFCDTSPILALSCTDTYNT
 55 EILIFIIVGSTLMVSLFTISASYVFILFTILKINSTSGKQKAFSTCVSHLLGVTFYSTLIFTYLPKPK
 SYSLGRDQVASVFYTIVIPVLNPLIYSLRNKEVKNAVIRVMQRRQDSR (SEQ ID NO: 393)

TTAACTTGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT
 TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTTGGCTGACATGGCCTTGGATCGGTAC
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTTGCCAACAGC
 TGGCATCTATCTCCTGGCTCAGTGGTTTGGCTAGTTCCTTAATCCATGCAACTTTTACCTTG
 5 CAATTGCCTCTCTGTGGCAACCATAGGCTGGACCATTTTATTTGCGAAGTACCAGCTCTTCT
 CAAGTTGGCTTGTGTGGACACCACTGTCAATGAATTGGTGCTTTTTTGTGTTAGTGTTCTGT
 TTGTTGTCATTCCACCAGCACTCATCTCCATCTCCTATGGCTTCATAACTCAAGCTGTGCTG
 AGGATCAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGCTCCTCCCACCTTACAG
 TGGTGATTATATTCTATGGCACCATAATCTACGTGTACCTGCAACCTAGTGACAGCTATGC
 10 CCAGGACCAAGGGAAGTTTATCTCCCTCTTCTACACCATGGTGACCCCCACTTTAAATCCT
 ATCATCTATACCTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAACTTCTCTCGGGA
 AAATTGTGA (SEQ ID NO: 398)

AOLFR214 sequences:

15 MDKSNSSVSEFVLLGLCSSQKLQLFYFCFFSVLYTVIVLGNLLIILTVTSDTSLHSPMYFLLGN
 LSFVDICQASFAATPKMIADFLSAHETISFSGCIAQIFFIHLFTGGEMVLLVSMAYDRYVAICKPLY
 YVIVMSRRCTCTVLMISWAVSLVHTLSQLSFTVNLPFCGPNVVDSEFFCDLPRVTKLACLDSEYIE
 ILIVVNSGILSLSTFSLVSSYIILVTWVWLKSSAAMAKAFSTLASHIAVVILFFGPCIFYVWPFTIS
 PLDKFLAIFYTVFTPVLPNIYTLNRNMDKAAVRKIVNHYLRPRRISEMSLVVVRTSFH (SEQ ID
 20 NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTACTGTTGGGACTCTGTAGTTCTC
 AAAAECTCCAGCTTTTCTATTTTGTCTTCTCTGTGTGTATACAGTCATTGTGCTGGGA
 AATCTTCTCATTATCCTCACAGTGACTTCTGATACCAGCTGCACTCCCCTATGTACTTTCT
 25 CTTGGGAAACCTTTCTTTGTGACATTTGTGAGGCTTCTTTTGCTACCCCTAAAATGATTG
 CAGATTTTCTGAGTGACACGAGACCATATCTTTCAGTGGCTGCATAGCCCAAATTTTCTTT
 ATTCACCTTTTACTGGAGGGGAGATGGTGCTACTTGTTCGATGGCCTATGACAGGTATG
 TAGCCATATGCAAACCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACTGTCTT
 GGTAATGATCTCCTGGGCTGTGAGCTTGGTGACACATTAAGCCAGTTATCATTACTGTG
 30 AACCTGCCTTTTGTGGACCTAATGTAGTAGACAGCTTTTTTTGTGATCTTCCTCGAGTCAC
 CAAACTTGCCCTGCCTGGACTCTTACATCATTGAAATACTAATTGTGGTCAATAGTGGAATT
 CTTTCCCTAAGCACTTTCTCTCTTGGTCAGCTCCTACATCATTATTCTTGTACAGTTTG
 GCTCAAGTCTTCAGCTGCAATGGCAAAGGCATTTTCTACGCTGGCTTCCCATATTGCAGTA
 GTAATATTATTCTTTGGACCTTGACATCTTCTATGTGTGGCCCTTACCATCTCTCCTTT
 35 GGATAAATTTCTGCCATATTTACACTGTTTTCACCCCGTCCTAAACCCCATTTATTTATA
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAAGGAAAATTGTGAACCATTACCTGAGGC
 CAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCCTTTCATTAA (SEQ ID NO:
 400)

AOLFR215 sequences:

40 MAHTNESMVSEFVLLGLSNSWGLQLFFFAIFSIVYVTSVLGNVLIIVISFDSHLNSPMYFLLSNL
 SFIDICQSNFATPKMLVDFFIERTISFEGCMAQIFVLHSFVGSEMMLLVAMAYDRFIAICKPLH
 YSTIMNRRLCVIFVSISWAVGLHSVSHLAFTVDLPFCGPNEVDSEFFCDLPLVIELACMDTYEM
 EIMTLTNSGLISLSCFLALISYTIILIGVRCRSSSGSSKALSTLTAHITVVILFFGPCIFYFIWPF SRL
 45 PVDKFLSVFYTVCTPLLNPPIYSLRNEDVKAAMWKLNRNHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT
 GGGGACTTCAACTTTTCTTTTTCGCCATCTTCTCTATAGTCTATGTGACATCAGTGCTAGGC
 AATGTCTTAATTATTGTCAATTATTTCTTTTGAATCCTTGAATCTCCTATGTACTTCTTG
 50 CTCAGTAATCTTTCTTTTATTGATATCTGTGAGTCTAACTTTGCCACCCCCAAGATGCTTGT
 AGACTTTTTTATTGAGCGCAAGACTATCTCCTTTGAGGGTTGCATGGCCAGATATTCGTT
 CTTACAGTTTTTGTGGGAGTGAGATGATGTTGCTTGTAGCTATGGCATATGACAGATTTA
 TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTCTGTGTAATTTT
 TGTGTCTATTTCTGGGCGGTGGGCGTTCTTCATTCTGTGAGCCACTTGGCTTTTACAGTGG
 55 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTTTGTGACCTTCCCTTGGTGATA
 GAGCTGGCTTGCATGGATACATATGAAATGGAAATTATGACCCTAACGAACAGTGCCCTG

ATATCATTGAGCTGTTTCCTGGCTTTAATTATTTCTACACCATCATTTTGATCGGTGTCCG
 ATGCAGGTCTCCAGTGGGTCACTAAGGCTCTTTCTACATTAAGTGGCCACATCACAGTG
 GTCATTCTTTCTTCGGGCCTTGCACTTATTTCTATATATGGCCTTTTAGCAGACTTCCTGT
 GGACAAATTTCTTTCTGTGTTCTACACTGTTTGTACTCCCTTGTGAACCCCATCATCTACT
 5 CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAACT
 CCTGGAAAACTAG (SEQ ID NO: 402)

AOLFR216 sequences:

MDVGNKSTMSSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNLIVITVIVDPLHSPMYFLL
 10 TNLISIIMSLASFATPKMITDYLTHKTI SFDGCLTQIFLHLFTGTEIILLMAMSFDRYIAICKPL
 HYASVISPVQVCVALVVASWIMGVMHMSQVIFALTLPCGPYEVDSSFFCDLPVVFQLACVDY
 VLGLFMISTSGIHALSCFIVLNSYVIVLVTVKHSSRGSSKALSTCTAHFIVVFLFFGPCIFIYMW
 PLSSFLTDKILSVFYTIPTLNPPIYTLRNQEVKIAMRKLNRLNFKAMPS (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTTGTTTTGCTGGGGCTCTCTAATTCCT
 GGGAACTACAGATGTTTTCTTTATGGTGTTCATTGCTTTATGTGGCAACAATGGTGGG
 TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCTCACCTACACTCTCCTATGTATTTCC
 TGCTTACCAATCTTTCAATCATTGATATGTCTCTTGCTTCTTCGCCACCCCAAAGATGATT
 ACAGATTACCTAACAGGTCACAAAACCATCTCTTTTGATGGCTGCCTTACCCAGATATTCT
 20 TTCTCCACCTTTTCACTGGAAGTATGATCATCTTACTCATGGCCATGTCTTTGATAGGTAT
 ATTGCAATATGCAAGCCCTGCACTATGCTTCTGTCTATTAGTCCCCAGGTGTGTGTTGCTCT
 CGTGGTGGCTTCCTGGATTATGGGAGTTATGCATTCAATGAGTCAGGTGCATTTTGCCCTC
 ACGTTACCATTTCTGTGGTCCCTATGAGGTAGACAGCTTTTTCTGTGACCTTCCTGTGGTGT
 CCAGTTGGCTTGTGTGGATACTTATGTTCTGGGCCCTCTTTATGATCTCAACAAGTGGCATA
 25 ATTGCGTTGCTCTGTTTTATTGTTTTATTAAATTCATATGTTATTGCTCTGGTTACTGTGAA
 GCATCATTTCTCCAGAGGATCATCTAAGGCCCTTTCTACTTGTACAGCTCATTTTCATTGTTG
 TCTTCTTGTCTTTGGGCCATGCATCTTCATCTACATGTGGCCACTAAGCAGCTTTCTCACA
 GACAAGATTCTGTCTGTGTTTTATACCATCTTTACTCCCACTCTGAACCCAAATAATCTATAC
 TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAACTGAAAAATAGGTTTCTAAATTT
 30 TAATAAGGCAATGCCTTCATAG (SEQ ID NO: 404)

AOLFR217 sequences:

MLESFQKSEQMAWSNQSAVTEFILRLSSSLELQIFYFLFFSIVYAATVLGNLLIVVTIASEPHLH
 SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAI SFE GCMTQMFFLHLLGGAIEVLLISM SFD
 35 RYVAICKPLHYLTIMSRMCVGLVILSWIVGIFHALSQLAFTVNLPFCGPNEVDSSFFCDLP LVIK
 LACVDYILGVFMISTSGMIALVCFILLVISYTHLVTVRQRSSGGSSKALSTCSAHFTVVT LFFGP
 CTFIYVWPFTNFPIDKVL SVFYTIYTPLLNPVIYTVRNKDV KYSMRKLS SHIFKSRKTDHTP
 (SEQ ID NO: 405)

40 ATGCTAGAGTCCTTCCAGAAATCAGAGCAAATGGCCTGGAGCAATCAGTCTGCGGTAACC
 GAATTCATACTACGGGGTCTGTCCAGTTCTTTAGAACTCCAGATTTTCTACTTCCTGTTTTT
 CTCCATAGTCTATGCAGCCACTGTGCTGGGGAACCTTCTTATTGTGGTCACCATTGCATCA
 GAGCCACACCTTCATTCCCCACGTACTTTCTGCTGGGCAATCTCTCCTTCATTGACATGTC
 CCTGGCCTCATTTGCCACCCCAAAATGATTGCAGACTTCCTTAGAGAACACAAAGCCATC
 45 TCTTTTGAAGGCTGCATGACCCAGATGTTCTTCTACATCTCTTAGGGGGTGTGAGATTG
 TACTGCTGATCTCCATGTCTTTGATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA
 ACAATCATGAGCCGAAGAATGTGTGTTGGGCTTGTGATACTTTCTGGATTGTCGGCATCT
 TCCATGCTCTGAGTCAGTTAGCATTTACAGTGAATCTGCCCTTCTGTGGACCCAATGAAGT
 AGACAGTTTCTTTGTGACCTCCCTTTGGTGATTAAACTTGCTTGTGTGCGACACATATATTC
 50 TGGGGGTGTTTCATGATCTCAACCAGTGGCATGATTGCCCTGGTGTGCTTCATCCTCTTGGT
 GATCTCTTACACTATCATCCTGGTCACCGTTCGGCAGCGTTCCTCTGGTGGATCCTCCAAA
 GCCCTCTCCACGTGCAGTGCCCACTTTACTGTTGTGACCCTTTTCTTTGGCCCATGCACTTT
 CATTTATGTGTGGCCTTTACAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA
 TATACACTCCCCTCTTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATTC
 55 CATGAGGAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA
 (SEQ ID NO: 406)

AOLFR218 sequences:

METANYTKVTEFVLTGLSQTREVQLVLFVIFLSFYLFILPGNIICTIRLDPHLTSPMYFLLANLA
 LLDIWYSSITAPKMLIDFFVERKIIISFGGCIQFLFLHFVGASEMFLIVMAYDRYAAICRPLHYA
 5 TIMNRRLLCCILVALSWMGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
 ICSSGLISVVCFIALLMSYAFLLALLKKHSGSDENTNRAMSTCYSHITIVVLMFGPSIYIYARPD
 SFSLDKVVSVFHTVIFPLLNPIIYTLRNKEVKAAMRKVVTKYILCEEK (SEQ ID NO: 407)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
 10 GGGAGGTCCAACCTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
 AATATCCTTATCATTTGACCATCAGGCTAGACCCTCATCTGACTTCTCCTATGTATTTCTCT
 GTTGGCTAATCTGGCCCTCCTTGATATTTGGTACTCTTCCATTACAGCCCCCTAAAATGCTCA
 TAGACTTCTTTGTGGAGAGGAAGATAATTTCCCTTTGGTGGATGCATTGCACAGCTCTTCTT
 CTTACACTTTGTTGGGGCTTCGGAGATGTTCTTGCTCATAGTGATGGCCTATGACCGCTAT
 15 GCTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCGACGTCTCTGCTGTATCCT
 GGTGGCTCTCTCCTGGATGGGGGGCTTCATTCTATAATACAGGTGGCTCTCATTGTT
 CGACTTCTTTCTGTGGGCCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTG
 TCCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCT
 GATCTCTGTGGTGTGTTTCATTGCTCTGTTAATGTCCTATGCCTTCCTTCTGGCCTTGCTCA
 20 AGAAACATTACAGGCTCAGATGAGAATACCAACAGGGCCATGTCCACCTGCTATTTCCACAT
 TACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCAT
 TTTCCCTAGATAAAGTGGTGTCTGTGTTTCATACTGTAATATTCCCTTTACTTAATCCCAT
 ATTTACACATTGAGAAACAAGGAAGTAAAGGCCATGAGGAAGGTGGTCACCAAATAT
 ATTTTGTGTGAAGAGAAGTGA (SEQ ID NO: 408).

AOLFR219 sequences:

MLTSLTDLCSPIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSSRELQPFLFLTFSLLYLAILLGNF
 LIILTVTSDSRLHTPMYFLLANLSFIDVCVASFATPKMIADFLVERKTISFDACLAQIFFVHLFTGS
 EMVLLVSMAYDRYVAICKPLHYMTVMSRRVCVVLVLISWVFGFIHTTSQLAFTVNLFPFCGP
 30 KVDSEFCDLPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVSYTVILVTVRNRSSASMAKAR
 STLTAHITVVTLLFGPCIFIYVWPFSSYSVDKVLAVFYTIFTLLNPVIYTLRNKEVKAAMSKLKS
 RYLKPSQVSVIRNVLFLETK (SEQ ID NO: 409).

ATGCTCACTTCATTAAGTATCTCTGTTTCTCTCCTATTCAGGTAGCTGAAATTAAGTCCCT
 35 TCCAAAATCGATGAATGAGACAAATCATTCTCGGGTGACAGAATTTGTGTGCTGGGACTG
 TCTAGTTCAAGGGAGCTCCAACCTTTCTTGTTTCTTACATTTTCACTACTTTATCTAGCAAT
 TCTGTTGGGCAACTTTCTCATCATCCTCACTGTGACCTCAGATTCCCGCCTTCACACCCCCA
 TGTACTTTCTGCTTGCAAACCTGTCATTTATAGACGTATGTGTTGCCTCTTTTGCTACCCCT
 AAAATGATTGCAGACTTTCTGGTTGAGCGCAAGACTATTTCTTTTGATGCCTGCCTGGCCC
 40 AGATTTCTTTGTTTCATCTCTTCACTGGCAGTGAAATGGTGCTCCTAGTTCCATGGCCTAT
 GACCGTTATGTTGCTATATGCAAACCTCTCCACTACATGACAGTCATGAGCCGTCGTGTAT
 GTGTTGTGCTCGTCCTCATTTTCATGGTTTGTGGGCTTCATCCATACTACCAGCCAGTTGGCA
 TTCCTGTTAATCTGCCATTTTGTGGTCCTAATAAGGTAGACAGTTTTTCTGTGACCTTCC
 TCTAGTGACCAAGTTAGCCTGCATAGACACTTATGTTGTGACCTTACTAATAGTTGCAGAT
 45 AGTGGCTTTCTTTCTCTGAGTTCTTTCTCCTCTTGTTGTCTCCTACACTGTGAATACTTGT
 ACAGTTAGGAATCGCTCCTCTGCAAGCATGGCGAAGGCCCGCTCCACATTGACTGCTCACA
 TCACTGTGGTCACCTTATTCTTTGGACCATGCATTTTCATCTATGTGTGGCCCTTCAGCAGT
 TACTCAGTTGACAAAGTCCTTGCTGTATTCTACACCATCTTCACGCTTATTTTAAACCCTGT
 AATCTACACGCTAAGAAACAAGAAAGTGAAGGCAGCTATGTCAAACTGAAGAGTCGGTA
 50 TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCTAGAAACAAAGTAA
 (SEQ ID NO: 410).

AOLFR220 sequences:

MKQYSVGNQHSNYRSLFPFLCSQMTQLTASGNQTMVTEFLFSMFPHAHRGGLLFFIPLLLIYG
 55 FILTGNLIMFIVIQVGMALHTPLYFFISVLSFLEICYTTTTIPKMLSCLISEQKSISVAGCLLQMYFF
 HSLGITESCULTAMAIDRYIAICNPLRYPTIMPKLICIQLTVGSCFCGFLVLPEIAWISTLPFCGS

NQIHQIFCDFTPVLSLACTDTFLVVIIVDAIHAAEIVASFLVIALSYIRIIIVILGMHSAEGHHKAFST
CAAH LAVFLFFGSVAVMYLRF SATYSVFWDTAIAVTFVILAPFFNPIIYSLKNKDMKEAIGRLF
HYQKRAGWAGK (SEQ ID NO: 411).

5 ATGAAGCAATATTTCAGTGGGTAATCAACATTCCAATTATAGGAGTCTCTTGTTTCCTTTTCT
GTGTTACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAATGGTGACTGAGTTCCT
CTTCTCTATGTTCCCGCATGCGCACAGAGGTGGCCTCTTATTCTTTATTCCCTTGCTTCTCA
TCTACGGATTATCCTAACTGGAAACCTAATAATGTTTCATTGTCATCCAGGTGGGCATGGC
CCTGCACACCCCTTTGTATTTCTTTATCAGTGTCTCTCCTTCCTGGAGATCTGCTATACCA
10 CAACCACCATCCCCAAGATGCTGTCCTGCCTAATCAGTGAGCAGAAGAGCATTTCGGTGGC
TGGCTGCCTCCTGCAGATGTACTTTTCCACTCACTTGGTATCACAGAAAGCTGTGTCTG
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAACCATCA
TGATTCCCAAACCTTTGTATCCAGCTGACAGTTGGATCCTGCTTTTGTGGCTTCCTCCTGTG
CTTCCTGAGATTGCATGGATTTCACCTTGCTTTCTGTGGCTCCAACCAGATCCACCAGAT
15 ATTCTGTGATTTACACCTGTGCTGAGCTTGGCCTGCACAGATACATTCTAGTGGTCATT
GTGGATGCCATCCATGCAGCGGAAATGTAGCCTCCTTCTGGTCATTGCTCTATCCTACA
TCCGGATTATTATAGTGATTCTGGGAATGCAGCTCAGCTGAAGGTCATCACAAGGCCTTTTC
CACCTGTGCTGCTCACCTTGCTGTGTTCTTGCTATTTTTTGGCAGTGTGGCTGTCATGTATT
TGAGATTCTCAGCCACCTACTCAGTGTTTTGGGACACAGCAATTGCTGTCACTTTTGTATC
20 CTTGCTCCCTTTTTCAACCCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA
TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGGAAATAG (SEQ ID NO:
412).

AOLFR221 sequences:

25 MRNLSGGHVEEFVLVGFPTTPPLQLLLFVLFFAIYLLTLENALIVFTIWLAPSLHRPMYFFLGH
LSFLELWYINVTIPRLAFLTQDGRVSYVGCMTQLYFFIALACTECVLLAVMAYDRYLAICGP
LLYPSLMPSSLATRLAAASWGSFFSSMMKLLFISQLSYCGPNIINHFFCDISPLNLTCSDEKA
ELVDFLLALVMILLPLLAVVSSYTAIIAILRIPTSRGRHKAFSTCAHLAVVVIYSSSTLFTYAR
PRAMYT FNHNKIIISVLYTHVPPFNPAIYCLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID
30 NO: 413).

ATGAGAAATTTGAGTGGAGGCCATGTCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC
CTCCCCTCCAGCTGCTCCTCTTTGTCCTTTTTTTTGCAATTTACCTTCTGACATTGTTGGAGA
ATGCACTTATTGTCTTCACAATATGGCTTGCTCCAAGCCTTCATCGTCCCATGTACTTTTTC
35 CTTGGCCATCTCTCTTTTCTGGAGCTATGGTACATCAATGTCACCATTCCTCGGCTCTTGGC
AGCCTTTCTTACCCAGGATGGTAGAGTCTCCTACGTAGGTTGCATGACCCAACTGTACTTC
TTTATTGCCTTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGCTACCT
GGCCATCTGTGGACCCCTCCTTTACCCTAGTCTCATGCCTTCCAGTCTGGCCACTCGCCTTG
CTGCTGCCTCTTGGGGCAGTGGCTTCTTCAGCTCCATGATGAAGCTTCTTTTTATTTCCTCAA
40 TTGTCCTACTGTGGACCCAACATTATCAACCACTTTTCTGTGATATTTCCCACTACTCAA
CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCCTTCTGGCCCTGGTGATG
ATTCTACTCCCTCTATTGGCTGTGGTTTCATCATACACTGCCATCATTGCAGCCATCCTGAG
GATCCCTACGTCCAGGGGACGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG
GTTGTTATCTACTACTCCTCCACTCTCTTACCTATGCACGGCCCCGGGCCATGTACACCTT
45 CAACCACAACAAGATTATCTCTGTGCTCTACACTATCATTGTACCATTCTTCAACCCAGCCA
TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGGCCTTCAGGAAGACAGTGATGGGCAGAT
GTCATATCCTAGGGATGTTTCAGGACTGA (SEQ ID NO: 414).

AOLFR222 sequences:

50 MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVTLSNVFIIIAIRLDSHLHTPMYFLSFL
SFSETCYTLGIIPRMLSGLAGGDQAISYVGCAAQMFFSASWACTNCFLLAAMGFDRYVAICAPL
HYASHMNP TLCAQLVITSFLTGYLFGLGMLTVIFHLSFCSSSHEIQHFFCDTPPVLSLACGDTGPS
ELRIFILSLVLLVSFFITISYAYILAILRIPSAEGQKKAFTSCASHLTVVIIHYGCASFVYLRPK
ASYSLERDQLIAMTYTVVTPLLNPVYSLRTRAIQTALRNAFRGRLLGKG (SEQ ID NO: 415).

55

ATGGGGCAGACCAACGTAACCTCCTGGAGGGATTTTGTCTTCCTGGGCTTCTCCAGTTCTG
GGGAGTTGCAGCTCCTTCTCTTTGCCCTGTTCCTCTCTCTGTATCTAGTCACTCTGACCAGC
AATGTCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCATGTACCTCTT
CCTTTCTCTCTATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAATGCTCT
5 CTGGCCTGGCTGGGGGGGACCAGGCTATCTCCTATGTGGGCTGTGCTGCCAGATGTTCTT
TTCTGCCTCATGGGCCTGTACTAACTGCTTCCTTCTGGCTGCCATGGGCTTTGACAGATATG
TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCCTCTGTGCCCAGCT
GGTCATTACTTCTTCTGACTGGATACCTCTTTGGACTGGGAATGACACTAGTTATTTTCC
ACCTCTCATTCTGCAGCTCCCATGAAATCCAGCACTTTTTTTGTGACACGCCACCTGTGCTG
10 AGCCTAGCCTGTGGAGATACAGGCCCCGAGTGAGCTGAGGATCTTTATCCTCAGTCTTTTGG
TCCTCTTGGTCTCCTTCTTCTTCATCACCTCTCCTACGCCTACATCTTGGCAGCAATACTG
AGGATCCCCCTCTGCTGAGGGGCAGAAGAAGGCCTTCTCCACTTGTGCCTCGCACCTTACAG
TGGTCATTATTCAATTATGGCTGTGCTTCCTTCGTGTACCTGAGGCCCAAAGCCAGCTACTCT
CTTGAGAGAGATCAGCTTATTGCCATGACCTATACTGTAGTGACCCCCCTCCTTAATCCCA
15 TTGTTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGAG
ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).

AOLFR223 sequences:

MEANESSEGISFVLLGLTTPGQQRPLFVLFLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA
20 HLSFADLCFASVTPKMLANLLAHDHSISLAGCLTQMYFFALGVTDSCLLAAMAYDCYVAIR
HPLPYATRMSRAMCAALVGMALVSHVHSLLYILLMARLSFCASHQVPHFFCDHQPLRLSC
SDTHHIQLLIFTEGAAVVVTPFLLILASYGAIAAAVLQLPSASGRRLRAVSTCGSHLAVVSLFYGT
VIAVYFQATSRREA EWGRVATVMYTVVTPMLNPIIYSLWNRDVQALRALLIGRRISASDS
(SEQ ID NO: 417).

25 ATGGAGGCTGCCAATGAGTCTTCAGAGGGAATCTCATTTCGTTTTATTGGGACTGACAACAA
GTCCTGGACAGCAGCGGCCTCTCTTTGTGCTGTTCTTGCTCTTGTATGTGGCCAGCCTCCTG
GGTAATGGACTCATTGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT
TCCTGCTGGCCACCTGTCCTTTGCTGACCTCTGTTTCGCCTCCGTCACTGTGCCAAAGATG
30 TTGGCCAACTTGTGGCCCATGACCACTCCATCTCGCTGGCTGGCTGCCTGACCCAAATGT
ACTTCTTCTTTGCCCTGGGGGTAAGTATAGCTGTCTTCTGGCGGCCATGGCCTATGACTG
CTACGTGGCCATCCGGCACCCCTCCCTATGCCACGAGGATGTCCCGGGCCATGTGCGCA
GCCCTGGTGGGAATGGCATGGCTGGTGTCCCACGTCCACTCCCTCCTGTATATCCTGCTCA
TGGCTCGCTTGTCTTCTGTGCTTCCACCAAGTGCCCCACTTCTTCTGTGACCACCAGCCT
35 CTCTTAAGGCTCTCGTGCTCTGACACCCACCACATCCAGCTGCTCATCTTCACCGAGGGCG
CCGAGTGGTGGTCACTCCCTTCCTGCTCATCTCGCTCCTATGGGGCCATCGCAGCTGC
CGTGCTCCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGGCTGTGTCCACCTGTGGCTCCAC
CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCATTGCAGTCTACTTCCAGGCCACATCCC
GACGCGAGGCAGAGTGGGGCCGTGTGGCCACTGTCATGTACACTGTAGTCACCCCATGC
40 TGAACCCCATCATCTACAGCCTCTGGAATCGGATGTACAGGGGGCACTCCGAGCCCTTCT
CATTGGGCGAAGGATCTCAGCTAGTGACTCCTGA (SEQ ID NO: 418).

AOLFR224 sequences:

MGSFNTSFEDGFILVGFSDWPQLEPILFVFIFIFYSLTFLGNTIIIALSWLDLRLHTPMYFFLSHL
45 LDLCFTTSTVPQLLINLCGVDRITRGGCVAQLFIYLALGSTECVLLVVMADFDRYA AAVCRPLHY
MAIMHPHLCQTLAIASWGAGFVNLSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT
EAKMFVARVIVVAVPAALILGSYVHIAHAVLRVKSTAGRRKAFGTGSHLLVFLFYGSAIYT
YLQSIHNYSEREGKFVALFYTIITPILNPLIYTLRNKDVKGALWKVLWRGRDSG (SEQ ID NO:
419).

50 ATGGGAAGTTTCAACACCAGTTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATTGGC
CGCAACTGGAGCCCATCCTGTTTGTCTTTATTTTATTTTCTACTCCCTAACTCTCTTTGGC
AACACCATCATCATCGCTCTCTCCTGGCTAGACCTTCGGCTGCACACACCTATGTACTTCTT
TCTCTCTCATCTGTCCCTCCTGGACCTCTGCTTCACCACCAGCACCGTGCCCCAGCTCCTGA
55 TCAACCTTTGCGGGGTGGACCGCACCATACCCGTGGAGGGTGTGTGGCTCAGCTCTTCAT
CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCCTGGTGGTGTATGGCCTTTGACCGCTAT

GCTGCTGTCTGTCGTCCACTCCACTACATGGCCATCATGCACCCCATCTCTGCCAGACCCCT
 GGCTATCGCCTCCTGGGGTGCGGGTTTCGTGAACCTCTCTGATCCAGACAGGTCTCGCAATG
 GCCATGCCTCTCTGTGGCCATCGACTGAATCACTTCTTCTGTGAGATGCCTGTATTTCTGAA
 GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCCGAGTCATAGT
 5 CGTGGCTGTTCCTGCAGCACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG
 AGGGTGAAGTCAACGGCTGGGCGCAGAAAGGCTTTTGGGACTTGTGGGTCCCACCTCCTA
 GTAGTTTTCTTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATTATTC
 TGAGCGTGAGGGAAAATTTGTTGCCCTTTTTATACTATAATTACCCCCATTCTCAATCCTC
 TCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGAGGG
 10 GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

AOLFR225 sequences:

MENYNQTSTDFILLGLFPPSIIDLFFFILIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID
 LNYISTIVPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLASMAYDRYIAICFPLHYLIRM
 15 SKRVCVLMITGWSIIGSINACAHTVYVHLHIPYCRSRAINHFFCDVPAMVTLACMDTWVYEGTV
 FLSATIFLVFPFIGISCSYGQVLFVAVYHMKSAEGRKKAYLTCSTHLTVVTFYAPFVYTYLRPRS
 LRSPTEDKVLAVFYTLTPMLNPIIYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).

ATGGAAAATTACAATCAAACATCAACTGATTTTCATCTTATTGGGGCTGTTTCCACCATCAA
 20 TAATTGACCTTTTCTTCTTCTCATTCTCATTGTTTTTCATTTTCCTGATGGCTCTAATTGGAAACC
 TGTCCATGATTCTTCTCATCTTCTTGGACACCCATCTCCACACACCCATGTATTTCTACTG
 AGTCAGCTCTCCCTCATTGACCTAAATTACATCTCCACCATTTGTTCTAAGATGGCATCTGA
 TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTCAGAGTTTCTTCTTCT
 TGGCATTAGGAGGTGCAGAAGCACTACTTTTGGCATCTATGGCCTATGATCGTTACATTGC
 25 TATTTGCTTTCTCTCCACTATCTCATCCGCATGAGCAAAAGAGTGTGTGTGCTGATGATA
 ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTACTCCATA
 TTCCTTATTGCCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCAGCAATGGTGACT
 CTGGCCTGCATGGACACCTGGGTCTATGAGGGCACAGTGTTTTTGAGTGCCACCATCTTTC
 TCGTGTTTCCCTTCTTGGTATTTTCATGTTTCTATGGCCAGGTTCTCTTTGCTGTCTACCAC
 30 ATGAAATCTGCAGAAGGGAGGAAGAAAGCCTATTTGACCTGCAGCACCCACCTCACTGTA
 GTAACTTTCTACTATGCACCTTTTGTCTACACTTATCTACGTCCAAGATCCCTGCGATCTCC
 AACAGAGGACAAGGTTCTGGCTGTCTTCTACACCATCTCACCCCAATGCTCAACCCCATC
 ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGGCCTGACACGAGTGAGTCAGAGAATC
 TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).

35

AOLFR226 sequences:

MEWRNHSGRVSEFVLLGFPAPAPLQVLLFALLLLAYVLVLTENTLIIMAIRNHSTLHKPMYFFL
 ANMSFLEIWYVTVTIPKMLAGFVGSQDHGQLISFEGCMTQLYFFLGLGCTECVLLAVMAYD
 RYMAICYPLHPYVIVSGRLCVQMAAGSWAGGFGISMVKVFLISGLSYCGPNIINHFFCDVSPLL
 40 NLSCTDMSTAELTDFILAIFILLGPLSVTGASYVAITGAVMHISSAAGRYKAFSTCASHLTVVIF
 YAASIFIYARPKALSAFDTNKLVSPLYAVIVPLLNPIIYCLRNQEVKRALCCTLHLYQHQPDP
 KKASRN (SEQ ID NO: 423).

ATGGAGTGCGGAACCATAGTGAGGAGAGTGAGTGAGTTTGTGTTGCTGGGCTTCCCTGCT
 45 CCTGCGCCACTACAGGTACTATTGTTTGCCCTTTTGTGCTGGCCTATGTGTTGGTGCTGAC
 TGAGAACACACTCATCATTATGGCAATTAGGAACCATCTACCTCCACAAACCCATGTAC
 TTTTTCTAGCTAATATGTCCTTTCTGGAGATCTGGTATGTCACTGTCACTATTCCCAAGAT
 GCTTGCTGGCTTTGTTGGATCCAAACAGGATCATGGACAGCTAATCTCCTTTGAGGGATGC
 ATGACACAGCTCTACTTTTCTTGGCTTGGGCTGCAGTGAGTGTGCTTCTCGCTGTTAT
 50 GGCCTATGATCGCTATATGGCCATCTGCTATCTCTCCACTACCCAGTCATTGTCAAGTGCC
 GGCTGTGTGTGCAGATGGCTGCTGGCTCTTGGGCTGGAGGTTTTGGCATCTCCATGGTCAA
 AGTTTTTCTTATTTCTGGCCTCTCTTACTGTGGCCCCAACATCATCAACCACTTTTTCTGTG
 ATGTCTCTCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTT
 ATCCTGGCCATTTTTATTCTTCTAGGGCCACTCTCTGTCACTGGGGCCTCCTATGTGGCCAT
 55 TACTGGTGCTGTGATGCACATATCTTCGGCTGCTGGACGCTATAAGGCCTTTTCCACCTGT
 GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCAGCCAGTATCTTCATCTATGCTCGGCC

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTACTGTATGCTGTCATTGTA
CCATTGCTCAATCCCATCATTTACTGCCTGCGCAATCAAGAGGTCAAGAGAGCCCTATGCT
GTACTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA
G (SEQ ID NO: 424).

5

AOLFR227 sequences:

MEPQNTSTVTNFQLLGFQNLLEWQALLFVIFLLIYCLTIIGNVVITTVVSQGLRLHSPMYMFLQH
LSFLEVWYTTSTVPLLLANLLSWGQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP
LRYPFMLHRGLCARLVVSWCTGVSTGFLHSMMSRLDFCGRNQINHHFCDLPPLMQLSCSRV
10 YITEVTIFILSIAVLCICFFLTLPYVFIVSSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMISMVY
CPSPHLLPEINKIISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKCGILWSTSKRKF
LY (SEQ ID NO: 425).

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTCAGCTGTTAGGATTCCAGAACCTTC
15 TTGAATGGCAGGCCCTGCTCTTTGTCATTTTCCTGCTCATCTACTGCCTGACCATTATAGGG
AATGTTGTCATCATCACCGTGGTGAGCCAGGGCCTGCGACTGCACTCCCCTATGTACATGT
TCCTCCAGCATCTCTCCTTTCTGGAGGTCTGGTACACGTCCACCACTGTGCCCTTCTCCTA
GCCAACCTGCTGTCTCGGGGCCAAGCCATCTCCTTCTCTGCCTGCATGGCACAGCTCTACT
TCTTCGTATTCTCGGCGCCACCGAGTGCTTTCTCCTGGCCTTCATGGCCTATGACCGTTAC
20 CTGGCCATCTGCAGCCCACTCCGCTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGTT
GGTGGTGGTCTCATGGTGCACAGGGGTCAGCACAGGCTTTCTGCATTCCATGATGATTTC
AGGTTGGACTTCTGTGGGCGCAATCAGATTAACCATTCTTCTGCGACCTCCCGCCACTCA
TGCAGCTCTCCTGTTCCAGAGTTTATATCACCGAGGTGACCATCTTCATCCTGTCAATTGCC
GTGCTGTGCATTTGTTTTTTCTGACACTGGGGCCCTATGTTTTTCATTGTGTCTCCATATT
25 GAGAATCCCTTCCACCTCTGGCCGGAGAAAGACCTTTTCCACATGTGGCTCCCACCTGGCT
GTTGTCACTCTCTACTACGGGACCATGATCTCCATGTATGTGTGTCCCAGTCCCCACCTGTT
GCCTGAAATCAACAAGATCATTTCTGTCTTCTACACTGTGGTCACACCACTGCTGAACCCA
GTTATCTACAGCTTGAGGAACAAAGACTTCAAAGAAGCTGTTAGAAAGGTCATGAGAAGG
AAATGTGGTATTCTATGGAGTACAAGTAAAGGAAGTTCCTTTATTAG (SEQ ID NO: 426).

30

AOLFR229 sequences:

MFYVNQIPFQLYHISFVYPTELWSRAIIPCMPTLSFWVCSATPVSPGFFALILLVFVTSIASNVVK
IILIHDSRLHTPMYFLLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYTLGAE
FFLLGLMSCDRYVAICNPLHYPDLMRSKICWLIVAAAWLGGSIDGFLTPVTMQPFCASREIN
35 HFFCEVPALLKLSCTDTSAYETAMYVCCIMMLLPFSVISGSYTRILITVYRMSEAEGRRKAVAT
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVTGALQK
VVGRCVSSGKVTTT (SEQ ID NO: 427).

ATGTTTTATGTAAATCAGATACCTTTCCAACCTTTATCATATCTCTTTCTGTACCCTACAGA
40 GCTATGGAGCAGAGCAATTATCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCA
ACGCCCCGTTTCCCCTGGCTTCTTTGCCCTCATTCTCCTGGTCTTGTGACCTCCATAGCCAG
CAACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTC
CTGCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCAAAATGCT
GGTCGACCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCACTGCCAACACTTC
45 CTCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCTGTGATCGCTA
CGTAGCCATCTGCAACCCTCTGCACTATCCTGACCTCATGAGCCGCAAGATCTGCTGGTTG
ATTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCACCA
TGCAGTTCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTT
CTGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGTGTATTA
50 TGATGCTCCTCATCCCTTCTCTGTGATCTCGGGCTCTTACACAAGAATTCTCATTACTGTT
TATAGGATGAGCGAGGCAGAGGGGAGGCGAAAGGCTGTGGCCACCTGCTCCTCACACATG
GTGGTTGTGACCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA
CACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTCACTCCCATGCTCAAT
CCACTCATTTACAGCCTTAGGAACAAGGATGTACGGGGGCCCTACAGAAGGTTGTTGGG
55 AGGTGTGTGCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).

AOLFR230 sequences:

MGMEGLLQNSTNFVLTGLITHPAFPGLLFAIVFSIFVVAITANLVMILLIHMDSR LHTPMYFLLS
 QLSIMDTIYICITVPKMLQDLLSKDKTISFLGCAVQIFLYLTLIGGEFFLLGLMAYDRYVAVCNP
 LRYPLLMNRRVCLFMVVGSWVGGSLDGFMLTPVTMSFPFCRSREINHFFCEIPAVLKLSDTDS
 5 LYETLMYACCVLMLLIPLSVISVSYTHILLTVHRMNSEAEGRRKAFATCSSHIMVVS VFYGAIFY
 TNVLPHSYHTPEKDKVVS AFYTILTPMLNPLIYSLRNKDVA AALRKVLGRCGSSQSIRVATVIR
 KG (SEQ ID NO: 429).

ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTTCGTCCTCACAGGCCTCATCACCC
 10 ATCCTGCCTTCCCCGGGCTTCTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA
 GCCAACTTGGTCATGATTCTGCTCATCCACATGGACTCCCGCCTCCACACACCCATGTACTT
 CTTGCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCCAAGATGC
 TCCAGGACCTCCTGTCCAAGGACAAGACCATTTCCTTCTCTGGGCTGTGCAGTTCAGATCTT
 CCTCTACCTGACCCTGATTGGAGGGGAATTCTTCTCTGCTGGGTCTCATGGCCTATGACCGC
 15 TATGTGGCTGTGTGCAACCCTCTACGGTACCCTCTCCTCATGAACCGCAGGGTTTGCTTATT
 CATGGTGGTTCGGCTCCTGGGTGGTGGTTCCTTGGATGGGTTCATGCTGACTCCTGTCACT
 ATGAGTTTCCCCTTCTGTAGATCCCGAGAGATCAATCACTTTTTCTGTGAGATCCCAGCCGT
 GCTGAAGTTGTCTTGCACAGACACGTCACCTCTATGAGACCCTGATGTATGCCTGCTGCGTG
 CTGATGCTGCTTATCCCTCTATCTGTATCTCTGTCTCCTACACGCACATCCTCCTGACTGT
 20 CCACAGGATGAACCTCTGCTGAGGGCCGGCGCAAAGCCTTTGCTACGTGTTCTCCACATT
 ATGGTGGTGAAGCTTTTCTACGGGGCAGCCTTCTACACCAACGTGCTGCCCCACTCCTACC
 AACTCCAGAGAAAAGATAAAGTGGTGTCTGCCTTCTACACCATCCTACCCCCATGCTCAA
 CCCACTCATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGG
 GAGATGTGGTTCTCCAGAGCATCAGGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID
 25 NO: 430).

AOLFR231 sequences:

MERANHSVSEFILLGLSKSQNLQILFFLGFSVVFVGVILGNLLILVTVTFDSSLHTPMYFLLSNL
 SCIDMILASFATPKMIVDFLRERKTISWWGCYSQMFFMHLLGGSEMMLLVAMAIDRYVAICKP
 30 LHYMTIMSPRVL TGLLLSSYAVGVHSSSQMAFMLTLPFCGPNVIDSFFCDLPLVIKLACKDTYI
 LQLLVIADSGLLSLVCFLLLLVSYGVHFSVRYRAASRSSKAFSTLSAHITVTLFFAPCVFIYVW
 PFSRYSVDKILSVFYTIFTPLLNPIIYTLRNQEVKAAIKKRLCI (SEQ ID NO: 431).

ATGGAAAGAGCAAACCATT CAGTGGTATCGGAATTTATTTTGTGGGACTTTCCAAATCTC
 35 AAAATCTTCAGATTTTATTCTTCTTGGGATTCTCTGTGGTCTTCGTGGGGATTGTGTTAGGA
 AACCTGCTCATCTTGGTGACTGTGACCTTTGATTTCGCTCCTTCACACACCAATGTATTTCT
 GCTTAGCAACCTCTCCTGCATTGATATGATCCTGGCTTCTTTTGCTACCCCTAAGATGATTG
 TAGATTTCTCCTCCGAGAACGTAAGACCATCTCATGGTGGGGATGTTATTCCCAGATGTTCTT
 TATGCACCTCCTGGGTGGGAGTGAGATGATGTTGCTTGTAGCCATGGCAATAGACAGGTAT
 40 GTTGCCATATGCAAACCCCTCCATTACATGACCATCATGAGCCCACGGGTGCTCACTGGGC
 TACTGTTATCCTCCTATGCAGTTGGATTTGTGCACTCATCTAGTCAAAATGGCTTTTCATGTTG
 ACTTTGCCCTTCTGTGGTCCCAATGTTATAGACAGCTTTTTCTGTGACCTTCCCCTTGTGAT
 TAAACTTGCCTGCAAGGACACCTACATCCTACAGCTCCTGGTCATTGCTGACAGTGGGCTC
 CTGTCACTGGTCTGCTTCTCCTCTTGTCTCTCCTATGGAGTCATAATATTCTCAGTTAG
 45 GTACCGTGCTGCTAGTCGATCCTCTAAGGCTTCTCCACTCTCTCAGCTCACATCACAGTTG
 TGACTCTGTTCTTTGCTCCGTGTGTCTTTATCTACGTCTGGCCCTTCAGCAGATACTCGGTA
 GATAAAATTCTTTCTGTGTTTACACAATTTTACACCTCTCTTAAATCTATTATTTATAC
 ATTAAGAAATCAAGAGGTAAAAGCAGCCATTA AAAAAAAGACTCTGCATATAA (SEQ ID NO:
 432).

AOLFR232 sequences:

MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV
 VIFVFLMALSGNAVILLIHCD AHLHTPMYFFISQLSLMDMAYISVTVPKMLLDQVMGVN KIS
 APECGMQMFFYVTLAGSEFFLLATMAYDRYVAICHPLRYPVLMNHRVCLFLSSGCWFLGSVD
 55 GFTFTPTMTFPFRGSREIHHFFCEVPAVLNLSCSDTSLYEIFMYLCCVLMMLIPVVISSSYLLILL

TIHGMNSAEGRKKAFATCSSHLTVVILFYGAAIYTYMLPSSYHTPEKDMMVSVFYTILTPVVPNP
LIYSLRNKDVMGALKKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTCGGATTTTCATCCTGATGGGAC
TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCCAACCACACTGGATG
GTCGGATTTTCATCCTGTTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG
GTCATTTTTGTGGTTTTCTGATGGCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACA
CTGTGACGCCACCTCCACACCCCCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACA
TGGCGTACATTTCTGTCACTGTGCCCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAA
10 GATCTCAGCCCCTGAGTGTGGGATGCAGATGTTCTTCTACGTGACACTAGCAGGTTTCAGAA
TTTTTCCTTCTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTA
CCCTGTCTCATGAACCATAGGGTGTGTCTTCTCTGTCATCAGGCTGCTGGTTCTCTGGGCT
CAGTGGATGGCTTCACATTCACCTCCCATCACCATGACCTTCCCCTTCCGTGGATCCCGGA
GATTCATCATTTCTTCTGTGAAGTTCCTGCTGTATTGAATCTCTCCTGCTCAGACACCTCAC
15 TCTATGAGATTTTCATGTACTTGTGCTGTCTCCTCATGCTCCTCATCCCTGTGGTGATCATT
TCAAGCTCCTATTTACTCATCTCTCCTCACCATCCACGGGATGAACCTCAGCAGAGGGCCGGA
AAAAGSCCTTTGCCACCTGCTCCTCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCC
ATCTACACCTACATGCTCCCCAGCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTG
TCTTCTATACCATCCTCACTCCAGTGGTGAACCTTTAATCTATAGTCTTAGGAATAAGGAT
20 GTCATGGGGGCTCTGAAGAAAATGTTAACAGTGAACCTGCCTTTCAAAAAGCTATGGAG
TAG (SEQ ID NO: 434).

AOLFR233 sequences:

25 MANITRMANHTGKLDIFILMGLFRSKHPALLSVVIFVFLKALSGNAVLILLIHCD AHLHSPMY
FFISQLSLMDMAYISVTPVKMLLDQVMGVNKVSAPECGMQMFLYLTLAGSEFFLLATMAYDR
YVAICHLRYPVLMNHRVCLFLASGCWFLGSDGFMLTPITMSFPFCRSWEIHFFCEVPAVTI
LSCSDTSLYETLMLYLCCVLMMLIPVTIISSSYLLILLTVHRMNSAEGRKKAFATCSSHLTVVILFY
GAAVYTYMLPSSYHTPEKDMMVSVFYTILTPVLNPLIYSLRNKDVMGALKKMLTVRFVL
(SEQ ID NO: 435).

30 ATGGCCAACATCACAGGATGGCCAACCACACTGGAAAGTTGGATTTTCATCCTCATGGGAC
TCTTCAGACGATCCAAACATCCAGCTCTACTTAGTGTGGTCATCTTTGTGGTTTTCTGAAG
GCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACACTGTGACGCCACCTCCACAGCC
CCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG
35 CCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAAGGTCTCAGCCCCTGAGTGTGGG
ATGCAGATGTTCTCTATCTGACACTAGCAGGTTTCGGAATTTTCCTTCTAGCCACCATGGC
CTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTACCCCTGTCTCATGAACCATAGG
GTCTGTCTTTCTCTGGCATCGGGCTGCTGGTTCTCTGGGCTCAGTGGATGGCTTCATGCTCAC
TCCCATCACCATGAGCTTCCCCTTCTGCAGATCCTGGGAGATTCATCATTTCTTCTGTGAAG
40 TCCCTGCTGTAAACGATCCTGTCTGCTCAGACACCTCACTCTATGAGACCCTCATGTACCTA
TGCTGTGTCCTCATGCTCCTCATCCCTGTGACGATCATTTCAAGCTCCTATTTACTCATCCT
CCTCACCGTCCACAGGATGAACCTCAGCAGAGGGCCGGAAGGAGGCTTTGCCACCTGCTC
CTCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCCGTCTACACCTACATGCTCCCCA
GCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCCTCACTCC
45 GGTGCTGAACCTTTAATCTATAGTCTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAA
ATGTTAACTGTGAGATTCGTCCTTTAG (SEQ ID NO: 436).

AOLFR234 sequences:

50 MPNSTVMFLLMRFSVDVWTLQILHSASFFMLYLVTLMGNILIVTVTTCDSSLHMPMYFFLRN
LSILDACYISVTPVTSVNSLLDSTTISKAGCVAQVFLVFFVYVELLFLTIMAHDYVAVCQPL
HYPVIVNSRICQMTLASLLSGLVYAGMHTGSTFQLPFCRSNVIHQFFCDIPSLKLSCSDTFSNE
VMIVVSALGVGGGCFIIRSYIHIFSTVLGFPRGADRTKAFSTCIPHILVSVFLSSCSSVYLRRP
AIPAATQDLILSGFYSIMPPLFNPIIYSLRNKQIKVAIKKIMKRIFYSENV (SEQ ID NO: 437).

55 ATGCCCAATTCAACCACCGTGATGGAATTTCTCCTCATGAGGTTTTCTGATGTGTGGACAC
TACAGATTTTACATTCTGCATCCTTCTTTATGTTGTATTTGGTAACTCTAATGGGAAACATC

CTCATTGTGACCGTCACCACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCCTCAG
GAATCTGTCTATCTTGGATGCCTGCTACATTTCTGTTACAGTCCCTACCTCATGTGTCAATT
CCCTACTGGACAGCACCACCATTTCTAAGGCGGGATGTGTAGCTCAGGTCTTCCTCGTGGT
TTTTTTGTATATGTGGAGCTTCTGTTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG
5 TCTGCCAGCCACTTCACTACCCTGTGATCGTGAACCTCTCGAATCTGCATCCAGATGACACT
GGCCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG
CCCTTCTGTGCGTCCAACGTTATTCATCAATTCTTCTGTGACATCCCCTCTCTGCTGAAGCT
CTCTTGCTCTGACACCTTCAAGCAATGAGGTCATGATTGTTGTCTCTGCTCTGGGGTAGGT
GGCGGCTGTTTCATCTTTATCATCAGGTCTTACATTACATCTTTTCGACCGTGCTCGGGTT
10 TCCAAGAGGAGCAGACAGAACAAAGGCCTTTTCCACCTGCATCCCTCACATCCTGGTGGTG
TCAGTCTTCCTCAGTTCATGCTCTTCTGTGTACCTCAGGCCACCTGCGATACCTGCAGCCAC
CCAGGATCTGATCCTTTCTGGTTTTTATTCCATAATGCCTCCCCTCTTTAACCCTATTATTTA
CAGTCTTAGAAATAAGCAAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAATTTTTTA
TTCAGAAAATGTGTAA (SEQ ID NO: 438).

15

AOLFR235 sequences:

MDGVNDSSLQGFVLMGISDHPQLEMIFFIAILFSYLLTLLGNSTIILSRLEARLHTPMYFFLSNL
SSLDLAFATSSVPQMLINLWGPCKTISYGGCITQLYVFLWLGATECILLVVMADFDRYVAVCRPL
RYTAIMNPQLCWLLAVIACLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL
20 NQAVLNGVCTFFTAVPLSIIVISYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVFLFYGSASYGY
LLPAKNSKQDQGKFISLFSYLVTPMVNPLIYTLRNMEVKGALRRLLGKGREVG (SEQ ID NO:
439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC
25 CCCAGCTGGAGATGATCTTTTTATAGCCATCCTCTTCTCCTATTTGCTGACCCTACTTGGG
AACTCAACCATCATCTTGCTTTCCCGCCTGGAGGCCCGGCTCCATACACCCATGTACTTCTT
CCTCAGCAACCTCTCCTCCTTGACCTTGCTTTGCTACTAGTTCAGTCCCCCAAATGCTGA
TCAATTTATGGGGACCAGGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT
CTTCCTTTGGCTGGGGGCCACCGAGTGCATCCTGCTGGTGGTGATGGCATTGACCGCTAC
30 GTGGCAGTGTGCCGGCCCCCTCCGCTACACCGCCATCATGAACCCCAAGCTCTGCTGGCTGC
TGGCTGTGATTGCCTGCCTGGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCCTCT
GCAGCTCCCATTGTGTGGGCACCGGAGGGTGGAGGGATTCTCTGCGAGGTGCCTGCCAT
GATCAAACTGGCCTGTGGCGACACAAGTCTCAACCAGGCTGTGCTCAATGGTGTCTGCACC
TTCTTCACTGCAGTCCCACTAAGCATCATCGTGATCTCCTACTGCCTCATTGCTCAGGCAGT
35 GCTGAAAATCCGCTCTGCAGAGGGGAGGCGAAAGGCGTTCAATACGTGCCTCTCCCATT
GCTGGTGGTGTTCCTCTTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGGCCAAGAAC
AGCAAAACAGGACAGGGCAAGTTCATTTCCTGTTTCTACTCGTTGGTCACACCCATGGTGA
ATCCCCTCATCTACACGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTTGCTGG
40 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

40

AOLFR236 sequences:

MTSQRDTAIYSINVSFVAKGMTSRVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL
LFLLIYSITVAGNLLILLTVGSDSHLSLPMYHFLGHSFLDACLSTVTVPKVMAGLLTLDGKVIS
FEGCAVQLYCFHFLASTEFLYTVMA YDRYLAICQLHYPVAMNRRMCAEMAGITWAIGATH
45 AAIHTSLTFRLLYCGPCHIA YFFCDIPPVLKACTDTTINELVMLASIGIVAAGCLILIVISYIFIVA
AVLRIRTAQGRQRAFPCTAQLTGVLLEYVPPVCIYLQPRSSEAGAGAPAVFYTIVTPMLNPFYI
TLRNKEVKHALQRLLCSSFRETAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCCATTAATGTCAGTTTTGTTGCAAAGG
50 GGATGAGTAGCCGCTCTGTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCAGA
CTGTGGTGAGCCACTTCTTCTGAGGGTTTGAGGTACACCGCTAAACATTCTAGCCTCTT
CTTCCTCCTCTTCTCCTCATCTACAGCATCACTGTGGCTGGGAATCTCCTCATCCTCCTAA
CTGTGGGCTCTGACTCTCACCTCAGCTTACCATGTACCACTTCTGGGGCACCTCTCCTTC
CTGGATGCCTGTTTGTCTACAGTGACAGTGCCCAAGGTCATGGCAGGCCTGCTGACTCTGG
55 ATGGGAAGGTGATCTCCTTTGAGGGCTGTGCCGTACAGCTTTATTGCTTCCACTTTCTGGC
CAGCACTGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

CCCCGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC
TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTCACCTTCCGCCTGCTCTACT
GTGGGCCTTGCCACATTGCCTACTTCTTCTGCGACATACCCCTGTCTAAAGCTCGCCTGT
ACAGACACCACCATTAATGAGCTAGTCATGCTTGCCAGCATTGGCATCGTGGCTGCAGGCT
5 GCCTCATCCTCATCGTTATTTCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA
GCCCAGGGCCGGCAGCGGGCCTTCTCCCCCTGCACTGCCAGCTCACTGGGGTGTCTCTGT
ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGC
CCCTGCTGTCTTCTACACAATCGTAACCTCAATGCTCAACCCATTCAATTTACACTTTGCGGA
ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAGCAGCTTCCGAGAGTCTACAG
10 CAGGCAGCCCACCCCATAG (SEQ ID NO: 442).

AOLFR237 sequences:

MDQRNYTRVKEFTFLGITQSRELSQVLFTFLFLVYMTTLMGNFLIMVTVTCESHLHTPMYFLL
RNLSILDICFSSITAPKVLIDLLSEKTIISFSGCVTQMFFFHLLGGADVFSLSVMAFDRIYIAISKPL
15 HYMTIMSRGRCTGLIVGFLGGGLVHSIAQISLLPLPVCGPVLDTFYCDVPQVLKLACTDTFT
LELLMISNNGLVSWFVFFLLISYTVILMMLRSHTGEGRRKAISTCTSHITVTVLHFVPCIYVYA
RPFTALPTDTAISVTFTVISPLLNPIHYTLRNQEMKMLAMRKLKRRLLGQSERILIQ (SEQ ID NO:
443).
20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCCTGGGAATTACTCAGTCCC
GAGAACTGAGCCAGGTCTTATTTACCTTCCTGTTTTTGGTGTACATGACAACTCTAATGGG
AAACTTCCTCATCATGGTTACAGTTACCTGTGAATCTCACCTTCATACGCCCATGTACTTCC
TGCTCCGCAACCTGTCTATTCTTGACATCTGCTTTTCTCCATCACAGCTCCTAAGGTCCTG
ATAGATCTTCTATCAGAGACAAAAACCATCTCCTTCAGTGGCTGTGTCACTCAAATGTTCT
25 TCTTCCACCTTCTGGGGGGGAGCAGACGTTTTTCTCTCTCTGTGATGGCGTTTGACCGCTAT
ATAGCCATCTCCAAGCCCCTGCACTATATGACCATCATGAGTAGGGGGCGATGCACAGGCC
TCATCGTGGGCTTCTGGGTGGGGGGCTTGCCACTCCATAGCGCAGATTTCTCTATTGCT
CCCACTCCCTGTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCAGGTCC
TCAAACCTGCCTGCACTGACACCTTCACTCTGGAGCTCCTGATGATTTCAAATAATGGGTT
30 AGTCAGTTGGTTTGTATTCTTCTTCTCCTCATATCTTACACGGTCATCTTGATGATGCTGA
GGTCTCACACTGGGGAAGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACCG
TGGTGACCCTGCATTTCTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCC
ACAGACACTGCCATCTCTGTCACTTCACTGTCTATCTCCCTTTGCTCAATCCTATAATTTA
CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAACTGAAGAGACGGCTAGGAC
35 AATCAGAAAGGATTTTAATTCAATAA (SEQ ID NO: 444).

AOLFR238 sequences:

MAPENFTRVTEFILTVSSCPQLPLFLVFLVLYVLTLMAGNLGIITLTSVDSRLQTPMYFFLRHL
AIINLGNSTVIAPKMLMNLVKKKTTSFYECATQLGGFLFFIVSEVMMLAVMAYDRIYVAICNP
40 LLYMVVSRRLCLLLVSLTYLYGFSTAIVVSPCIFSVSYCSSNIINHFCYCDIAPLLALSCSDTYIPE
TIVFISAATNLFSSMITVLVSFYFNIVLSILRIRSEGRKKAFTSCASHMIAVTVFYGTMLFMYLQP
QTNHSLDTDKMASVFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:
445).
45 ATGGCTCCTGAAAATTTACACAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC
CAGAGCTCCAGATTCCTCTTCTGGTCTTCTAGTGCTCTATGTGCTGACCATGGCAGG
GAACCTGGGCATCATCACCTCACCAGTGTTGACTCTCGACTTCAAACCCCATGTACTTTT
TCCTGAGACATCTAGCTATCATCAATCTTGGCAACTCTACTGTCAATTGCCCTAAAATGCTG
ATGAACTTTTGTAGTAAAGAGAAACTACCTCATTCTATGAATGTGCCACCAACTGGGAG
50 GGTCTTGTCTTTATTGTATCGGAGGTAATGATGCTGGCTGTGATGGCCTATGACCGCTA
TGTGGCCATTTGTAACCTCTGCTCTACATGGTGGTGGTGTCTCGGCGGCTCTGCCCTCTGC
TGGTGTCCCTCACGTACCTCTATGGCTTTTCTACAGCTATTGTGGTTTACCTTGTATATTC
TCTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTTTACTGTGATATTGCACCTCTGTT
AGCATTATCTTGCTCTGATACTTACATACCAGAAACAATAGTCTTTATATCTGCAGCAACA
55 AATTTGTTTTTTTCCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTTGTCCATTCTA
AGGATACGTTACACAGAAGGAAGGAAAAAGCCTTTTCCACCTGCGCTTCGCATATGATA

GCAGTCACGGTTTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT
 CACTGGATACTGATAAGATGGCTTCTGTGTTTTACACATTGGTGATTCCCTATGCTGAATCC
 CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAAT
 CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

5

AOLFR239 sequences:

MDPQNYSLVSEFVLHGLCTSRHLQNFFFIFFGVYVAIMLGNLLILVTVISDPCLHSSPMYFLLG
 NLAFLDMWLASFATPKMIRDFLSQKLISFGGCMQAIFLHFTGGAEMVLLVSMAYDRYVAIC
 KPLHYMTLMSWQTCIRLVLASWVGVFVHSISQVAFVNLPCGPNEVDSFFCDLPLVIKLACM
 10 DTYVLGIIMISDSGLLSLSCFLLLLISYTVILLAIRQRAAGSTSKALSTCSAHIMVVTLLFFGPCIFV
 YVRPFSRFSVDKLLSVFYTIFTPLLNPIIYTLRNEEMKAAMKKLQNRRTVFQ (SEQ ID NO: 447).

ATGGACCCACAGAACTATTCCTTGGTGTGAGAATTTGTGTTGCATGGACTCTGCACTTCAC
 GACATCTTCAAAATTTTTCTTTATATTTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT
 15 AACCTTCTCATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACTCCTCCCCTATGTACTT
 CCTGCTGGGGAACCTAGCTTTCTGGACATGTGGCTGGCCTCATTGCCACTCCCAAGATG
 ATCAGGGATTTCCTTAGTGATCAAAAACCTCATCTCCTTTGGAGGATGTATGGCTCAAATCT
 TCTTCTTGCACTTTACTGGTGGGGCTGAGATGGTGCTCCTGGTTTCCATGGCCTATGACAG
 ATATGTGGCCATATGCAAACCTTGCATTACATGACTTTGATGAGTTGGCAGACTTGCATC
 20 AGGCTGGTGTGCTGGCTTCATGGGTGCTGGATTGTGCACTCCATCAGTCAAGTGGCTTTCA
 CTGTAAATTTGCCTTACTGTGGCCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG
 GTGATCAAACCTTGCTGCATGGACACCTATGTCTTGGGTATAATTATGATCTCAGACAGTG
 GGTTGCTTTCCTTGAGCTGTTTTCTGCTCCTCCTGATCTCCTACACCGTGATCCTCCTCGCT
 ATCAGACAGCGTGCTGCCGGTAGCACATCCAAAGCACTCTCCACTTGCTCTGCACATATCA
 25 TGGTAGTGACGCTGTTCTTTGGCCCTTGCAATTTTGTGTTATGTGCGGCCCTTTCAGTAGGTT
 TCTGTGGACAAGCTGCTGTGTTTATACCATTTTACTCCACTCCTGAACCCCATAT
 CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAAACCGACGGGT
 GACTTTTCAATGA (SEQ ID NO: 448).

AOLFR240 sequences:

MAGENHTTLPFLLLGFSDLKALQGFLFWVVLVYLVTLLGNSLIILLTQVSPALHSPMYFFLR
 QLSVVELFYTTDIVPRTLNLGSPHPQAISFQGCAAQMYVFIVLGISECCLLTAMAYDRYVAIC
 QPLRYSTLLSPRACLAMVGSWLGTIATTHASLIFSLPFRSHPIIPHFLCDILPVLRLASAGKHR
 SEISVMTATIVFIMIPFSLIVTSYIRILGAILAMASTQSRRKVFSTCSSHLLVVSLLFFGTASITYIRPQ
 35 AGSSVTTDRVLSLFYTVITPMLNPIIYTLRNKDVRRALRHLVKRQRPS (SEQ ID NO: 449).

ATGGCTGGGGAAAACCATACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA
 AGGCCCTGCAGGGCCCCCTGTTCTGGGTGGTGCTTCTGGTCTACCTGGTCACCTTGCTGGG
 40 TAACCTCCCTGATCATCCTCCTCACACAGGTGAGCCCTGCCCTGCACTCCCCCATGTACTTCT
 TCCTGCGCCAACTCTCAGTGGTGGAGCTCTTCTACACCACTGACATCGTGCCAGGACCTT
 GGCCAAATCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCCAGATG
 TACGTCTTCATTGTCTGGGCATCTCGGAGTGCTGCCTGCTCACGGCCATGGCCTATGACC
 GATATGTTGCCATCTGCCAGCCCCACGCTATTCCACCCTCTTGAGCCCACGGGCCTGCTT
 GGCCATGGTGGGGTCTCCTGGCTCACAGGCATCATCACGGCCACCACCCATGCCTCCCTC
 45 ATCTTCTCTACCTTTTCGCAGCCACCCGATCATCCCGCACTTTCTCTGTGACATCCTGCC
 AGTACTGAGGCTGGCAAGTGCTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGCCAC
 CATAGTCTTCATTATGATCCCCTTCTCTCTGATTGTACCTCTTACATCCGCATCCTGGGTG
 CCATCCTAGCAATGGCCTCCACCCAGAGCCGCCGCAAGGTCTTCTCCACCTGCTCCTCCCA
 TCTGCTCGTGGTCTCTCTCTTTTGAACAGCCAGCATCACCTACATCCGGCCGAGGCA
 50 GGCTCCTCTGTTACCACAGACCGCGTCTCAGTCTCTTCTACACAGTCATCACACCCATGCT
 CAACCCCATCATCTACACCCTTCGGAACAAGGACGTGAGGAGGGCCCTGCGACACTGGT
 GAAGAGGCAGCGCCCCCTCACCTGA (SEQ ID NO: 450).

AOLFR241 sequences:

MPQILIFTYLNMFYFPPLQILAENLTMVTEFLLLGFSSLGEIQLALFVVFLFLYLVLSGNVTIIS
 55 VIHLDKSLHTPMYFFLGILSTSETFYTFVILPKMLINLLSVARTISFNCCALQMFFFLGFAITNCLL

LGVMGYDRYAAICHPLHYPTLMSWQVCGKLAACAIGGFLASLTVVNLVFSLPFCSANKVNH
YFCDISAVILLACTNTDVNEFVIFICGVLVLVVPFLFICVSYLCILRTLKIPSAEGRRKAFSTCAS
HLSVVIVHYGCASFIYLRPTANYVSNKDRLVTVTYITVPLLNPMVYSLRNKDVLQAIRKVLG
KKGSLKLYN (SEQ ID NO: 451).

5 ATGCCCCAAATTCTTATATTCACATACCTGAATATGTTTTACTTCTTTCCCCCTTTGCAGAT
CTTGGCAGAAAACCTCACCATGGTCACCGAATTCCTGTTGCTGGGTTTTTCCAGCCTTGGT
GAAATTCAGCTGGCCCTCTTTGTAGTTTTTCTTTTCTGTATCTAGTCATTCTTAGTGGCAA
TGTCACCATATCAGTGTCTACCTGGATAAAAGCCTCCACACACCAATGTACTTCTTCC
10 TTGGCATTCTCTCAACATCTGAGACCTTCTACACCTTTGTCATTCTACCCAAGATGCTCATC
AATCTACTTTCTGTGGCCAGGACAATCTCCTTCAACTGTTGTGCTCTTCAAATGTTCTTCTT
CCTTGGTTTTGCCATTACCAACTGCCTGCTATTGGGTGTGATGGGTATGATCGCTATGCTG
CCATTTGTCACCTCTGCATTACCCCACTCTTATGAGCTGGCAGGTGTGTGGAAAACCTGGC
AGCTGCCTGTGCAATTGGTGGCTTCTTGGCCTCTCTTACAGTAGTAAATTTAGTTTTAGCC
15 TCCCTTTTTGTAGCGCCAACAAAGTCAATCATTACTTCTGTGACATCTCAGCAGTCATTCTT
CTGGCTTGTACCAACACAGATGTTAACGAATTTGTGATATTCAATTTGTGGAGTTCTTGTAC
TTGTGGTTCCCTTTCTGTTTATCTGTGTTTCTTATCTCTGCATTCTGAGGACTATCCTGAAG
ATTCCCTCAGCTGAGGGCAGACGGAAGCGTTTTCCACCTGCGCCTCTCACCTCAGTGTTG
TTATTGTTCAATTATGGCTGTGCTTCTTCTACCTGAGGCCTACAGCAAACCTATGTGTCC
20 AACAAAGACAGGCTGGTGACGGTGACATACAGATTGTCACTCCATTACTAAACCCCATG
GTTTATAGCCTCAGAAACAAGGATGTCCAACCTGCTATCAGAAAAGTGTGGGCAAGAAA
GGTTCTCTAAACCTATATAATTGA (SEQ ID NO: 452).

AOLFR242 sequences:

25 MNTTLFHPYPSFLLGLIPGLESMLHWVGFPFFAVFLTAVLGNITILFVIQTDSSLHHPMFYFLAILS
SIDPGLSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESAVLVAMAYDCYVAICDPLCY
TLVLTKNVVSVMALAIFLRPLVFVIPFVLFILRLPFCGHQIIPHTYGEHMGARLSCASIRVNIY
LCAISILVFDIIAIVISYVQILCAVFLSSHDARLKAFSTCGSHVCVMLTFYMPAFFSMTHFRGR
NIPHFIHILLANFYVIPPALNSVIYGVRTKQIRAQVLKMFFNK (SEQ ID NO: 453).

30 ATGAATACCACTCTATTTTCATCCTTACTCTTTCTTCTGGAATTCCTGGGCTGGAAAG
TATGCATCTCTGGGTTGGTTTTCTTTCTTTGCTGTGTTCTGACAGCTGTCCTTGGGAATA
TCACCATCCTTTTTGTGATTGAGACTGACAGTAGTCTCCATCATCCCATGTTCTACTTCTG
GCCATTCTGTCTATTTGACCCGGGCTGTCTACATCCACCATCCCTAAAATGCTTGGCAC
35 CTTCTGGTTTACCCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCCAGATGTTCTTCTATCC
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC
CATCTGTGACCCTCTTTGCTACACGTTGGTGCTGACAAACAAGGTGGTGTGAGTTATGGCA
CTGGCCATCTTTCTGAGACCCTTAGTCTTTGTCTATACCTTTGTTCTATTTATCCTAAGGCT
TCCATTTTGTGGACACCAAATTATTCCTCATACTTATGGTGAGCACATGGGCATTGCCCCG
40 CTGTCTGTGCCAGCATCAGGGTAAACATCATCTATGGCTTATGTGCCATCTCTATCCTGGT
CTTTGACATCATAGCAATTGTCAATTCCTATGTACAGATCCTTTGTGCTGTATTTCTACTCT
CTTCACATGATGCACGACTCAAGGCATTGACGACCTGTGGCTCTCATGTGTGTGTCATGTT
GACTTCTATATGCCTGCATTTTTCTCATTATCATGACCCATAGGTTTGGTCGGAATATACCTC
ACTTTATCCACATTCTTCTGGCTAATTTCTATGTAGTCATTCCACCTGCTCTCAACTCTGTA
45 ATTTATGGTGTGAGAACCAAACAGATTAGAGCACAAGTGCTGAAAATGTTTTTCAATAAAT
AA (SEQ ID NO: 454).

AOLFR243 sequences:

MEQVNKTVVREFVVLGFSSRLARLQQLLFVIFLLLYLFTLGTNAIIISTIVLDRALHTPMYFFLAIL
SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFGSSHSFLAAMGYDRYMAICNPLR
50 YSVLMGHGVCMLMAAACAGFTVSLVTTSLVFHLPFHSSNQLHHFFCDISPVLKLASQHS
SQLVIFMLGVFALVPLLLLVSYIRIISAILKIPSSVGRYKTFSTCASHLIVVTVHYSASFYLRPK
TNYTSSQDTLISVSYTILTPLFNPMIYSLRNKEFKSALRRITIGQTFYPLS (SEQ ID NO: 455).

55 ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTCGTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCTGCTCCTCTACCTGTTCACTCTGGGCACC

5 AATGCAATCATCATTTCCACCATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT
CCTTGCCATCCTTTCTTGCTCTGAGATTTGCTATACCTTTGTCATTGTACCCAAGATGCTGG
TTGACCTGCTGTCCCAGAAGAAGACCATTCTTTTCTTGCTGGGCTGTGCCATCCAAATGTTTCC
TTCCTCTTCTTTGGCTCCTCTCACTCCTTCCTGCTGGCAGCCATGGGCTATGATCGCTATAT
10 GGCCATCTGTAACCCACTGCGCTACTCAGTGCTCATGGGACATGGGGTGTGTATGGGACTA
ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCTCCCTGGTCACCACCTCCCTAGTATTTC
TCTGCCCTTCCACTCCTCCAACCAGCTCCATCACTTCTTCTGTGACATCTCCCCTGTCCTTA
AACTGGCATCTCAGCACTCCGGCTTCAGTCAGCTGGTCATATTCATGCTTGGTGTATTTGC
CTTGGTCATTCCTCTGCTACTTATCCTAGTCTCCTACATCCGCATCATCTCTGCCATTCTAA
15 AAATCCCTTCCCTCCGTTGGAAGATACAAGACCTTCTCCACCTGTGCCTCCCATCTCATTTGTG
GTAAGTGTTCATAACAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATTACACTTC
AAGCCAAGACACCCTAATATCTGTGTCATACACCATCCTTACCCCATTTGTTCAATCCAATG
ATTTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAAACT
TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

15

AOLFR244 sequences:

20 MWQEYYFLNVFFLLKVCCLTINSHVVILLPWECYHLIWKILPYIGTTVGSMEEYNTSSDFTF
MGLFNRKETSGLIFAIJSIIFFALMANGVMIFLIQTDLRHLTPMYFLLSHLSLIDMMYISTIVPKM
LVNYLLDQRTISFVGCTAQHFLYLTLVGAEFFLLGLMAYDRYVAICNPLRYPVLMSSRRVCWMI
IAGSWFGGSLDGFLLPITMSFFPCNSREINHFCEAPVCLKACADTALYETVMYVCCVLMML
IPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTVVSIFYGAAMYTYMLPHSYHKPAQ
DKVLSVIFYTILTPMLNPLIYSLRNKDVGTALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

25 ATGTGGCAAGAATACTATTTTTTAAATGTTTTCTTCCCACTTTTAAAAGTTTGCTGCCTAAC
AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTGGAAGATAT
TACCTTATATCGGCACAACTGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT
CACTTTTCATGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTTGCCATCATCTCT
ATCATCTTCTTACCAGCACTGATGGCCAATGGGGTTATGATCTTCTGATCCAAACAGATT
30 TGCGCCTTCATACACCCATGTACTTCTCCTCAGCCACCTTTCCTTAATTGACATGATGTAT
ATTTCCACTATTGTGCCTAAGATGCTGGTTAATTACCTGCTGGATCAAAGGACCATTTCCTT
TGTGGGGTGCACAGCTCAACACTTCTCTACCTTACCCTTGTGGGAGCTGAATTCTTCTCTG
CTGGGCCTCATGGCCTATGACCGCTATGTGGCCATTTGCAACCTCTGAGATACCCTGTCC
TCATGAGCCGCCGGGTCTGTTGGATGATTATAGCAGGTTTCTGGTTTGGGGGCTCTTTGGA
TGGCTTCTCCTAACCCCATCACCATGAGCTTTCCTTCTGCAATTCCCGGGAGATTAACC
35 ACTTCTTCTGTGAGGCACCAGCAGTCCTGAAGTTGGCATGTGCAGACACAGCCCTCTACGA
GACAGTGATGTATGTGTGCTGTGTTTGTATGCTGCTGATTCTTCTCTGTAGTACCTTGCTT
CCTATGCCCGAATCCTGACTACAGTTCAGTGATGAGCTCAGTGAGGAGGAGGAGGAGGAGG
CATTTGCCACTTGCTCATCCACATGACTGTGGTGTCTTGTCTACGGGGGCTGCCATGTAC
ACCTACATGCTGCCACATTCTTACCACAAGCCAGCCAGGACAAAGTCTCTCTGTGTTTT
40 ACACCATTCTCACACCCATGCTGAACCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC
TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCTCAAAGGGTGTGAGGAGGTGT
CTTTTGA (SEQ ID NO: 458).

AOLFR245 sequences:

45 MDLKNGLSVTEFILLGFFGRWELQIFFFVTFSLIYGATVMGNILIMVTVTCRSTLHSPLYFLLGN
LSFLDMCLSTATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLIIIMAFDRYVAICKP
LHYRTIMSHKLLKGFAILSWIIGFLHSISQIVLTMNLPFCGHNVINNIFCDLPLVIKLACIETYTLE
LFVIADSGLLSFTCFILLVSYIVILVSVPKSSHGLSKALSTLSAHIIIVTLFFGPCIFIYVWPFFSL
ASNKTLAVFYTVITPLNPSIYTLRNKKMQEAIKRLRFQYVSSAQNF (SEQ ID NO: 459).

50

55 ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGGACGAT
GGGAACCTCAAATTTCTTCTTTGTGACATTTTCCCTGATCTACGGTGCTACTGTGATGGGA
AACATTCTCATTATGGTCACAGTGACATGTAGGTCAACCTTCATTCTCCCTTGTACTTTCT
CCTTGGAAATCTCTCTTTTTTGGACATGTGTCTCTCCACTGCCACAACACCCAAGATGATCA
TAGATTTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT
CATGCACTTCTTTGGGGGTGCTGAGATGACTCTTCTGATAATCATGGCCTTTGACAGGTAT

GTAGCCATATGTAAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG
 TTTGCGATACTTTTCATGGATAATTGGTTTTTTACACTCCATAAGCCAGATAGTTTTAAACAAT
 GAACTTGCCTTTCTGTGGCCACAATGTCATAAAACAACATATTTTGTGATCTTCCCCTTGTGA
 TCAAGCTTGCTTGCAATTGAAACATACACCCTGGAATTATTTGTCATTGCTGACAGCGGGCT
 5 GCTCTCTTTCACCTGTTTCATCCTCTTGCTTGTTCCTTACATTGTCATCCTGGTCAGTGTACC
 AAAAAAATCATCATATGGGCTCTCCAAGGCGCTGTCCACATTGTCTGCCCACATCATTGTG
 GTCACCTCTGTTCTTTGGACCTTGTAATTTTATCTATGTTTGGCCATTCAAGTAGTTTGGCAAG
 CAATAAAACTCTTGCCGTATTTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA
 CCCTGAGAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCGAATATGTTAGTT
 10 CTGCACAGAATTTCTAG (SEQ ID NO: 460).

AOLFR246 sequences:

MSPENQSSVSEFLLGLPIRPEQQAFFTLFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
 LALTDISFSSVTVPKMLMDMRKYKSILYBECISQMYFFIFFTDLDSFLITSMAFYDRYVAICHPL
 15 HYTVIMREELCVFLVAVSWILSCASSLSHTLLLRLSFCANTIPHVFCDLAALLKLSCSDIFLNE
 LVMFTVGVVVITLPMFICILVSYGYIGATILRVPSTKGIHKALSTCGSHLSVVSLEYGSIFGQYLF
 PTVSSSIDKDIVALMYTVVTPMLNPFYISLRNRDMKEALGKLFSRATFFSW (SEQ ID NO:
 461).

20 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTTCTGGGCCTCCCCATCCGGC
 CAGAGCAGCAGGCTGTGTTCTTCACCCTGTTCTGGGCATGTACCTGACCACGGTGTGGG
 GAACCTGCTCATCATGCTGCTCATCCAGCTGGACTCTACCTTCACACCCCCATGTACTTCT
 TCCTCAGCCACTTGGCTCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
 ATGGACATGCGGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTTCTCAGATGTATT
 25 TTTTATAATTTTTACTGACCTGGACAGCTTCCTTATTACATCAATGGCATATGACCGATAT
 GTTGCCATATGTACCCCTCTCCACTACACTGTCATCATGAGGGAAGAGCTCTGTGTCTTCTT
 AGTGGCTGTATCTTGGATTCTGTCTTGTGCCAGCTCCCTCTCTCACACCCTTCTCCTGACCC
 GGCTGTCTTTCTGTGCTGCGAACACCATCCCCCATGTCTTCTGTGACCTTGCTGCCCTGCTC
 AAGCTGTCCTGCTCAGATATCTTCTCAATGAGCTGGTCATGTTACAGTAGGGGTGGTGG
 30 TCATTACCCTGCCATTATGTGTATCCTGGTATCATATGGCTACATTGGGGCCACCATCCTG
 AGGGTCCCTTCAACCAAAGGGATCCACAAAGCATTGTCCACATGTGGCTCCCATCTCTCTG
 TGGTGTCTCTTATTATGGGTCAATATTTGGCCAGTACCTTTTCCCGACTGTAAGCAGTTCT
 ATTGACAAGGATGTCATTGTGGCTCTCATGTACACGGTGGTCACACCCATGTTGAACCCCT
 TTATCTACAGCCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAAACTCTTCAGTAGAG
 35 CAACATTTTCTCCTTGGTGACATCTGACTTTTAAAAAATTAG (SEQ ID NO: 462).

AOLFR247 sequences:

MGQHNLTVLTEFILMELTRRPELQIPLFGVFLVIYLLITVVGNLTMILTKLDSHLHTPMYFSIRHL
 ASVDLGNSTVICPKVLANFVVDNRNTISYYACAAQLAFFLMFIIEFFILSAMAYDRYVAICNPILL
 40 YYVIMSQRQLCHVLVGIQYLYSTFQALMFTIKIFTLTFCGSNVISHFYCDDVPLLPMLCSNAQEIE
 LLSILFSVFNLISSFLIVLVSYMLILLAICQMHSAGEGRKKAFTSTCGSHLTVVVVFYGSLLFMYMQ
 PNSTHFFDTDKMASVFYTLVIPMLNPLIYSLRNEEVKNAFYKLFEN (SEQ ID NO: 463).

45 ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAACCTCACAAGGCGGC
 CTGAGCTGCAGATTCCCCTTTTTGGAGTCTTCCTCGTCATCTACCTAATCACAGTGGTGGGC
 AACCTAACTATGATCATTTTGACCAAACCTGGACTCCCACTTACATACACCTATGTACTTTTC
 TATCAGACATTTGGCTTCTGTTGATCTTGGTAATTCTACTGTCAATTTGTCCCAAGGTGCTGG
 CAAATTTTGTGTGGATCGAAATACTATTTCTTATTATGCATGTGCTGCACAGCTGGCATTTC
 50 TTCCTTATGTTCAATTATCAGTGAATTTTTCATCCTGTGAGCCATGGCCTATGACCGCTATGT
 GGCCATTTGTAACCCCTCTGCTCTATTATGTTATTATGTCTCAGCGACTGTGTCACTGTACTGG
 TGGGCATTCAATATCTCTACAGCACATTTTCAGGCTCTGATGTTCACTATTAAGATTTTACA
 TTGACCTTCTGTGGCTCTAATGTGCATCAGTCATTTTACTGTGATGATGTTCTTGTGCTACC
 TATGCTTTGCTCAAATGCACAGGAAATAGAATTGTTGAGCATACTATTTTCTGTATTTAATT
 TGATCTCCTCCTTTCTGATAGTCTTAGTGTCTACATGTTGATTTTGTAGCTATATGTCAA
 55 ATGCATTCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTTCCCATTTGACAGTGG
 TGGTTGTGTTCTATGGGTCTCTACTCTTCATGTACATGCAGCCCAATCCCACTCACTTCTTT

GATACTGATAAAATGGCTTCTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCCTTTGAT
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTGA
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPALPTGGLLPHQHTMMEIANVSSPEVFLVLLGFSTRPSLETVLFIVVLSFYMVLSILNGI
IILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLG
ATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVGSSTLTMLLPLCG
NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIARAVLKIRSAEGR
10 RKAFTNCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTEVKS
ALRHMVLENCCGSAGKLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCACAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT
GATGGAAATAGCCAATGTGAGTTCTCCAGAAGTCTTTGTCCTCCTGGGCTTCTCCACACGA
15 CCCTCACTAGAACTGTCCTCTTCATAGTTGTCTTGAGTTTTTACATGGTATCGATCTTGGG
CAATGGCATCATCATTCTGGTCTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT
TTCTTGCCAACCTCCCCTTCTGGACATGAGCTTACCACGAGCATTGTCCACAGCTCCTG
GCTAACCTCTGGGGACCACAGAAAACCATAAGCTATGGAGGGTGTGTGGTCCAGTTCTAT
ATCTCCCATTTGGCTGGGGGCAACCGAGTGTGTCCTGCTGGCCACCATGTCTATGACCGCT
20 ACGCTGCCATCTGCAGGCCACTCCATTACACTGTCATTATGCATCCACAGCTTTGCCTTGG
GCTAGCTTTGGCCTCCTGGCTGGGGGGTCTGACCACCAGCATGGTGGGCTCCACGCTCACC
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTTCTTTGCGAGATGCCCCCTCA
TTATGCAACTGGCTGTGTGGATACCAGCCTCAATGAGATGGAGATGTACCTGGCCAGCTT
TGTCTTTGTGTCTGCTCTGGGGCTCATCTGGTCTCTTACGGCCACATTGCCCGGGCCG
25 TGTGAAGATCAGGTCAGCAGAAAGGGCGGAGAAAGGCATTCAACACCTGTTCTTCCCACG
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTCATGTATCTCCAGCCAGCCAAGAG
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTTCTACACCGTAGTCACTCCTGCGCTG
AACCCTTATTTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGCACATGGTA
TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

30

AOLFR249 sequences:

MKSQIEKSDLKYRAILLQKVTRMFLFWVLLLVLRLVVMGRGNSTEVTEFHLLGFGVQHEF
QHVLFIVLLLIYVTSIGNIGMILLIKTDSRLQTPMYFFPQHAFVDICYTSAITPKMLQSFTEN
NLITFRGCVIQLVYATFATSDCYLLAIMAMDCYVAICKPLRYPMIMSQTVYIQLVAGSYIIGSI
35 NASVHTGFTFSLFCKSNKINHFFCDGLPILALSCSNIDINIILDVVFVGFDLMFTELVIIFSIIYIM
VTILKMSSTAGRKKSFTSCASHLTAVTIFYGTLSYMYLQPQSNNSQENMKVASIFYGTVIPMLN
PLIYSLRNKEGK (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAAGTGACTTAAAAATATAGAGCCATTTTATTGCAAAAAGTC
40 ACAAGGATGTTCTGCTTTTCTGGGTCCTTCTCTTGGTCCTTTCTAGACTTTTGGTAGTCAT
GGGTCGAGGAAACAGCACTGAAGTGACTGAATCCATCTTCTGGGATTTGGTGTCCAACAC
GAATTTACAGCATGTCCTTTTCAATTGACTTCTTCTTATCTATGTGACCTCCCTGATAGGAAA
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTTCAAACACCCATGTACTTTTTTC
CACAACATTTGGCTTTTGTGATATCTGTTATACTTCTGCTATCACTCCCAAGATGCTCCAA
45 AGCTTCACAGAAGAAAATAATTTGATAACATTTGCGGGCTGTGTGATACAATTCTTAGTTT
ATGCAACATTTGCAACCAGTGACTGTTACCTCCTAGCTATTATGGCAATGGATTGTTATGT
TGCCATCTGTAAGCCCCCTTCGCTATCCCATGATCATGTCCCAAACAGTCTACATCCAACCTCG
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTTACATTTTCA
CTGTCCTTCTGCAAGTCTAATAAAAATCAATCACTTTTTCTGTGATGGTCTCCCAATCTTGC
50 CCTTTCATGCTCCAACATTGACATCAACATCACTTCTAGATGTTGTCTTTGTGGGATTTGACT
TGATGTTCACTGAGTTGGTCATCATCTTTTCTACATCTACATTATGGTCACCATCTGAAG
ATGTCTTCTACTGCTGGGAGGAAAAATCCTTCTCCACATGTGCCTCCCACCTGACAGCAG
TAACCATTTTCTATGGGACACTCTCTTACATGTACTTACAGCCTCAGTCTAATAATTCTCAG
GAGAATATGAAAGTAGCCTCTATATTTATGGCACTGTTATTCCCATGTTGAATCCTTTAAT
55 CTATAGCTTGAGAAATAAGGAAGGAAAAATAA (SEQ ID NO: 468).

AOLFR250 sequences:

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLIILAIGSDLHLHTPMYFFLANLSFV
DMGLTSSTVTKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCY
STVMRPQVCALMLALCWVLTNIVALHTHFLMARLSFCVTGEIAHFFCDITPVLKLSGSDTHINE
5 MMVFVLGGTVLIVPFLCIVTSYIHIVPAILRVTRGGVGKAFSTCSSHLCVVCVFYGTLFSAAYLC
PPSIASEEKDIAAAAMYTIVTPMLNPFYISLRNKDMKGALKRFLSHRSIVSS (SEQ ID NO: 469).

ATGGAAAACCAATCCAGCATTTCTGAATTTTTCTCCGAGGAATATCAGCGCCTCCAGAGC
AACAGCAGTCCCTCTTCGGAATTTTCTGTGTATGTATCTTGTACCTTGACTGGGAACCTG
10 CTCATCATCTGGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTTTCTTGGC
CAACCTGTCTTTTGTGACATGGGTTTAAACGTCCTCCACAGTTACCAAGATGCTGGTGAAT
ATACAGACTCGGCATCACACCATCTCCTATACGGGTTGCCTCACGCAAATGTATTTCTTTCT
GATGTTTGGTGATCTAGACAGCTTCTTCCTGGCTGCCATGGCGTATGACCGCTATGTGGCC
ATTTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAATGCTTGC
15 ATTGTGCTGGGTCTCACCATAATCGTTGCCCTGACTCACACGTTTCTCATGGCTCGGTTGT
CCTTCTGTGTGACTGGGGAATTTGCTCACTTTTTCTGTGACATCACTCCTGTCCTGAAGCTG
TCATGTTCTGACACCCACATCAACGAGATGATGGTTTTTGTCTTGGGAGGCACCGTACTCA
TCGTCCCCTTTTATGCAATTGTACCTCCTACATCCACATTGTGCCAGCTATCCTGAGGGTC
CGAACCCTGGTGGGTGGGCAAGGCCTTTCCACCTGCAGTTCCACCTCTGCGTTGTTT
20 GTGTGTTCTATGGGACCTCTTCAGTGCCTACCTGTGTCTCCCTCCATTGCCTGAAGAG
AAGGACATTGCAGCAGCTGCAATGTACACCATAAGTACTCCCATGTTGAACCCCTTTATCT
ATAGCCTAAGGAACAAGGACATGAAGGGGGCCCTAAAGAGGCTCTTCAGTCACAGGAGTA
TTGTTTCCTCTTAG (SEQ ID NO: 470).

AOLFR251 sequences:

MEGNKTWITDITLPRFQVGPALILLGLFSAFYTLTLLGNGVIFGHIICLDCKLHTPMYFFLSHLA
IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFHVECLILVVMYSYDRYADICHPLRY
NILMSWRVCTVLAVASWVFSLLALVPLVLRLPFCGPHEINHFEILSVLKLACADTWLNQV
VIFAACVFILVGPLCLVLVSYLRLAAILRIQSGEGRRKAFSTCSSHLCVVGGLFFGSAIVTYMAPK
30 SRHPEEQQKVLSLFLNPNMLNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTTGGTCCA
GCACTGGAGATTCTCTCTGTGGACTTTTCTCTGCCTTCTATACACTCACCTTGCTGGGGAA
TGGGGTCATCTTTGGGATTATCTGCCTGGACTGTAAGCTTCACACACCCATGTACTTCTTCC
35 TCTCACACCTGGCCATTGTTGACATATCCTATGCTTCCAACATATGTCCCAAGATGCTGACG
AATCTTATGAACCAGGAAAGCACCATCTCCTTTTTTCCATGCATAATGCAGACATTCTTGT
ATTTGGCTTTTGTCTACGTAGAGTGTCTGATTTTGGTGGTGATGTCTATGATCGCTATGCG
GACATCTGCCACCCCTTACGTTACAATATCCTCATGAGCTGGAGAGTGTGCACTGTCCTGG
CTGTGGCTTCTGCGGGCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCTCAAGTT
40 GGCCTGTGCTGACACCTGGCTCAACCAGGTGGTCATCTTGCAGCCTGCGTGTTTCATCCTG
GTGGGGCCACTCTGCCTGGTGCTGGTCTCCTACTTGCGCATCCTGGCCGCCATCTTGAGGA
TCCAGTCTGGGGAGGGCCGCAGAAAGGCCTTCTCCACCTGCTCCTCCACCTTTGCGTGGT
GGGACTCTTCTTTGGCAGCGCCATTGTACGTACATGGCCCCCAAGTCCCGCCATCCTGAG
45 GAGCAGCAGAAAGTTCTTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCTGA
TATATAGCCTAAGGAATGCAGAGGTCAAGGGCGCCCTGAGGAGGGCACTGAGGAAGGAG
AGGCTGACGTGA (SEQ ID NO: 472).

AOLFR252 sequences:

MRLANQTLGGDFLLGIFSQISHPGRLCLLIFSIFLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL
IDLTYISVTVPKMLVNQLAKDKTISVLGCGTQMYFYQLGGAECCLLAAMAYDRYVAICHPLR
YSVLSMHRVCLLLASGCWFVGSVDGFMLTPIAMSFPCRSHIEQHFFCEVPAVLKLSGSDTSLY
KIFMYLCCVIMLLIPVTVISVSYYYIILTIHKMNSVEGRKKAFTTCSHITVVSIFYGAAIYNYML
PSSYQTPEKDMMSFFYTILTPVLNPIHYSFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

ATGCGGCTGGCCAACCAGACCCTGGGTGGTGACTTTTTCTGTGGGAATCTTCAGCCAGA
TCTCACACCCTGGCCGCCTCTGCTTGCTTATCTTCAGTATATTTTTGATGGCTGTGTCTTGG
AATATTACATTGATACTTCTGATCCACATTGACTCCTCTCTGCATACTCCCATGTACTTCTT
TATAAACCAGCTCTCACTCATAGACTTGACATATATTTCTGTCACTGTCCCCAAAATGCTG
5 GTGAACCAGCTGGCCAAAGACAAGACCATCTCGGTCCTTGGGTGTGGCACCCAGATGTAC
TTCTACCTGCAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCCATGGCCTATGACCGCT
ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC
CTGGCATCAGGCTGCTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATCGCCA
TGAGCTTCCCCTTCTGCAGATCCCATGAGATTGAGCACTTCTTCTGTGAGGTCCCTGCTGTT
10 TTGAAGCTCTCTTGTCTCAGACACCTCACTTTACAAGATTTTCATGTACTTGTGCTGTGTCAT
CATGCTCCTGATACCTGTGACGGTCATTTCAAGTGTCTTACTACTATATCATCCTCACCATCC
ATAAGATGAAGTCAAGTGGAGGTGCGAAAAAGGCCTTCACCACCTGCTCCTCCACATTAC
AGTGGTCAGCCTCTTCTATGGAGCTGCTATTTACAACATACATGCTCCCCAGCTCCTACCAA
ACTCCTGAGAAAGATATGATGTCATCCTTTTTCTACACTATCCTTACACCTGTCTTGAATCC
15 TATCATTTACAGTTTCAGGAATAAGGATGTCACAAGGGCTTGAAGAAAAATGCTGAGCGT
GCAGAAACCTCCATATTAA (SEQ ID NO: 474).

AOLFR253 sequences:

MTFFSSGGNCEPVMCSGNQTSQNQTASTDFTLTGLFAESKHAALLYTVTFLLFLMALTGNALL
20 ILLIHSEPRLHTPMYFFISQLALMDLMLYLCVTPVKMLVGQVTGDDTISPSGCGIQMFFHLTLAG
AEVFLLAAMAYDRYAAVCRPLHYPLLMNQVRVQLLVSAWVLMVDGLLLTPITMSFPFCQS
RKILSFFCETPALLKLSGSDVSLYKMLTYLCCILMLLTPIMVISSSYTLILHLIHRMNSAAGRRKA
LATCSSHMIIVLLLFGASFYTYMLRSSYHTAEQDMMVSAFYTIFTPVLNPLIYSLRNKDVTRAL
RSMQMQRMNQEK (SEQ ID NO: 475).

25 ATGACTTTTTTTCTCAGGGGGAAACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT
CTCAGAATCAAACAGCAAGCACTGATTTACCCCTCACGGGACTCTTTGCTGAGAGCAAGCA
TGCTGCCCTCCTCTACACCGTGACCTTCCTTCTTTCTTGATGGCCCTCACTGGGAATGCCC
TCCTCATCCTCCTCATCCACTCAGAGCCCCGCCTCCACACCCCCATGTACTTCTTCATCAGC
30 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCCAAGATGCTTGTGGGCC
AGGTCACCTGGAGATGATACCATTTCCCCGTCAGGCTGTGGGATCCAGATGTTCTTCCACCT
GACCCTGGCTGGAGCTGAGGTTTCTCCTGGCTGCCATGGCCTATGACCGATATGCTGCT
GTTTGCAGACCTCTCCATTACCCACTGCTGATGAACCAGAGGGTGTGCCAGCTCCTGGTGT
CAGCCTGCTGGGTTTTGGGAATGGTTGATGGTTTGTGCTCACCCCCATTACCATGAGCTT
35 CCCCTTTTGCCAGTCTAGGAAAATCCTGAGTTTTTCTGTGAGACTCCTGCCCTGCTGAAGC
TCTCCTGCTCTGAGCTCTCCCTCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT
CTCACCCCCATCATGGTCTATCTCCAGCTCATACACCCCTATCCTGCATCTCATCCACAGGAT
GAATTCTGCCGCCGCCGCGCAGGAAGGCCTTGGCCACCTGCTCCTCCACATGATCATAGTG
CTGCTGCTCTTCGGTGCTTCCTTCTACACCTACATGCTCCGGAGTTCTACCACACAGCTGA
40 GCAGGACATGATGGTGTCTGCCTTTTACACCATCTTCACTCCTGTGCTGAACCCCCCTATTT
ACAGTCTCCGCAACAAAGATGTCACCAGGGCTCTGAGGAGCATGATGCAGTCAAGAATGA
ACCAAGAAAAGTAG (SEQ ID NO: 476).

AOLFR254 sequences:

45 MTNTSSSDFTLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI
MDTLFICTTVPKLLADMVSKEKIIISFVACGIQIFLYLTMIGSEFFLLGLMAYDCYVAVCNPLRYP
VLMNRKKCLLLAAGAWFGGSLDGFLLPITMNVPCGSRSSINHHFCEIPAVLKLACADTSLYET
LMYICCVLMLLIPISIISTSYSLILLTIHRMPSAEGRKAFTTCSHLTVVSIFYGAAFYTYVLPQS
FHTPEQDKVVSIFYTIVTPMLNPLIYSLRNKDVIGAFKKVFACSSAQKVATSDA (SEQ ID NO:
50 477).

ATGACGAACACATCATCCTCTGACTTCACCCTCCTGGGGCTTCTGGTGAACAGTGAGGCTG
CCGGGATTGTATTTACAGTGATCCTTGCTGTTTTCTTGGGGGCCGTGACTGCAAAATTTGGT
CATGATATTCTTGATTCAAGTGGACTCTCGCCTCCACACCCCCATGTACTTTCTGCTCAGTC
55 AGCTGTCCATCATGGACACCCTTTTATCTGTACCACTGTCCCAAACTCCTGGCAGACAT
GGTTTCTAAAGAGAAGATCATTTCTTTGTGGCCTGTGGCATCCAGATCTTCTCTACCTG

ACCATGATTGGTTCTGAGTTCTTCCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT
CTGTAACCCTCTGAGATACCCAGTCTTGATGAACCGCAAGAAGTGTCTTTTGCTGGCTGCT
GGTGCTGGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCACCATGAATGTCC
CTTACTGTGGCTCCCGAAGTATCAACCATTTTTTCTGTGAGATCCCAGCAGTTCTGAAACT
5 GGCCTGTGCAGACACGTCCTTGATGAAACTCTGATGTACATCTGCTGTGCTCATGTTG
CTCATCCCCATCTCTATCATCTCCACTTCCTACTCCCTCATCTTGTTAACCATCCACCGCAT
GCCCTCTGCTGAAGGTCGAAAAAGGCCTTCACCACTTGTTCTCCCACTTGACTGTAGTT
AGCATCTTCTATGGGGCTGCCTTCTACACATACGTGCTGCCCCAGTCCTTCCACACCCCCG
AGCAGGACAAGAGTGTGACGCCTTCTATACCATTGTACGCCCCATGCTTAATCCTCTCAT
10 CTACAGCCTCAGAAACAAGGACGTCATAGGGGCATTAAAAAGGTATTGTCATGTTGCTCA
TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

AOLFR255 sequences:

MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKIILIHIDSLHTPMYFLLSQLS
15 LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH
YPVLMRSRKICWLIVAAAWLGGSIDGFLTPVTMQPFCASREINHFFCEVPALLKLSCTDTSAY
ETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRGKAVATCSSHMVVVSLFYGAAMYT
YVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQKVVGRCVSSGKVTF (SEQ
ID NO: 479).

20 ATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTTCAGCAACG
CCCGTTTCCCCTGGCTTCTCTTTGCCCTCATTCTCCTGGTCTTTTGGACCTCCATAGCCAGC
AACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTCCCT
GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTCCACCATTGTGCCCCAAATGCTG
25 TCGACCCAGGTGATGAGCCAGAGAGCCATTTCCTTTGCTGGATGCAGTGCCTCAACACTTCC
TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCCTATGATCGCTAC
GTAGCCATCTGCAACCTCTGCACTATCCTGTCTCATGAGCCGCAAGATCTGCTGGTTGA
TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCACCAT
GCAGTTCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTTC
30 TGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTAT
GATGCTCCTCATCCCTTTCTGTGCATCTCGGGCTCTTACACAAGAATTCTCATTACTGTTT
ATAGGATGAGCGAGGCAGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCTCACACATGG
TGGTTGTCAGCCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCAC
ACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTTACTCCCATGCTCAATC
35 CACTCATTTACAGCCTTAGGAACAAGGATGTACAGGGGCCCTACAGAAGGTTGTGGGGA
GGTGTGTGCTCCTCAGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

AOLFR256 sequences:

MGGKQPWVTEFILVGFQVGPALAILLCGLFSVFYTLTLGNGVIFGHIICLDSKLHTPMYFFLSHL
40 AIIDMSYASNNVPKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVVMYDRYVAICHPF
QYTVIMSWRVCTILASTCWIISFLMALVHITHILRPPFCGPQKINHFIQIMSVFKLACAGPRLNQ
VVLVYAGSAFIVEGPLCLELVSNLHILSRHLEDPMGRAADRLTLPAPSHLCMVGLLFGSTMVM
YMAPKSRHPPEEQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:
481).

45 ATGGGAGGCAAGCAGCCCTGGGTACAGAATTCATCCTGGTGGGATTCCAGGTTGGTCCA
GCACTGGCGATTCTCCTCTGTGGACTCTTCTGTCTTCTATACACTACCCCTGCTGGGGAA
TGGGGTCATCTTTGGGATTATCTGCCTGGACTCTAAGCTTCACACACCCATGTACTTCTTCC
TCTCACACCTGGCCATCATTGACATGTCCTATGCTTCCAACAATGTTCCCAAGATGTTGGC
50 AAACCTAATGAACCAGAAAAGCACCATCTCCTTTGTTCCATGCATAATGCAGACTTTTTTG
TATTTGGCTTTTGCTGTTACAGAGTGCCTGATTTTGGTGGTGTATGTCCTATGATAGGTATGT
GGCCATCTGCCACCTTTCCAGTACACTGTCATCATGAGCTGGAGAGTGTGCACGATCCTG
GCCTCAACATGCTGGATAATTAGCTTTCTCATGGCTCTGGTCCATATAACTCATATTCTGAG
GCCGCTTTTTGTGGCCACAAAAGATCAACCACTTTATCTGTCAAATCATGTCCGTATTCA
55 AATTGGCCTGTGCTGGCCCTAGGCTCAACCAGGTGGTCTATATGCGGGTTCTGCGTTCAT
CGTAGAGGGGGCCGCTCTGCCTGGAGCTGGTCTCCAACCTGCACATCCTGTGCGGCCATCTT

5 GAGGATCCAGTAATGGGGAGGGCCGCGAGACCGACTTACTCTTCCTGCTCCTTCCCACCTTT
GCATGGTGGGACTCCTTTTTTGGCAGCACCATGGTCATGTACATGGCCCCAAGTCCCGCCA
CCCTGAGGAGCAGCAGAAGGTCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC
CCCTTGATCTACAGCCTGAGGAACGAGAGGTCAAGGGTGCCCTGAAAAGAGTGTTGTGG
AAACAGAGATCAAAGTGA (SEQ ID NO: 482).

AOLFR257 sequences:

10 MESNQTWITEVILLGFQVDPALELFLFGFLLFYSLTLMGNGIILGLIYLD SRLHTPMYVFLSHL
AIVDMSYASSTVPKMLANLVMHKKVISFAPCILQTFLYLAFATECLILVMMCYDRYVAICHPL
QYTLIMNWRVCTVLASTCWIFSLLALVHITLILRLPFCGPQKINHFFCQIMSVFKLACADTRLN
QVVLFAGSFILVGPLCLVLVSYLHILVAILRIQS GEGRRKAFSTCSSHL CVVGLFFGSAIVMYM
APKSSHSQERRKILSLFYSLFNPILNPLIYSLRNAE VKGALKRVLWKQRSM (SEQ ID NO: 483).

15 ATGGAAAGCAATCAGACCTGGATCACAGAAGTCATCCTGTTGGGATTCCAGGTGGACCCA
GCTCTGGAGTTGTTCTCTTTGGGTTTTTCTTGCTATTCTACAGCTTAACCTGATGGGAAA
TGGGATTATCCTGGGGCTCATCTACTTGGACTCTAGACTGCACACACCCATGTATGTCTTC
CTGTCACACCTGGCCATTGTGGACATGTCCTATGCCTCGAGTACTGTCCCTAAGATGCTAG
CAAATCTTGTGATGCACAAAAAAGTCATCTCCTTTGCTCCTTGCATACTTCAGACTTTTTTG
TATTTGGCGTTTGCTATTACAGAGTGTCTGATTTTGGTGATGATGTGCTATGATCGGTATG
20 TGGCAATCTGTCAACCCCTTGCAATACACCCCTCATTATGAACTGGAGAGTGTGCACTGTCT
GGCTCAACTTGCTGGATATTTAGCTTTCTCTTGGCTCTGGTCCATATTACTCTTATTCTGA
GGCTGCCTTTTTGTGGCCACAAAAGATCAACCACTTTTTCTGTCAAATCATGTCCGTATTC
AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGTGGTCTATTTGCGGGTTCTGCGTTCA
TCTTAGTGGGGCCGCTCTGCCTGGTGTGCTGGTCTCCTACTTGCACATCCTGGTGGCCATCTTG
25 AGGATCCAGTCTGGGGAGGGCCG CAGAAAGGCCTTCTCTACCTGCTCCTCCACCTCTGCG
TGGTGGGGCTTTTTCTTTGGCAGCGCCATTGTGTCATGTACATGGCCCCCAAGTCAAGCCATT
TCAAGAACGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCCTGAACCCC
CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTCCTTTGGAAA
CAGAGATCAATGTGA (SEQ ID NO: 484).

30

AOLFR259 sequences:

35 MGDNQSRVTEFILVGFQLSVEMEVLFWIFSLLYLFSLLANGMILGLICLD PRLRTPMYFFLSHL
AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVVMYSYDRFVAICHPL
HYTVIMNWRVCTVLAITSWACGFS LALINLILLRLPFCGPQEVNHFFGEILSVLKLACADTWIN
EIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSKEGRKKAFTSCSSHL CVVGLYFGMAMVVY
LVPDNSQRQKQKILTLFYSLFNPLL NPLIYSLRNAQVKGALYRALQKKRTM (SEQ ID NO:
485).

40 ATGGGGGACAACCAATCACGGGTACAGAATTCATCCTGGTTGGATTCCAGCTCAGTGTG
GAGATGGAAGTGCTCCTCTTCTGGATCTTCTCCCTGTTATATCTCTTCAGCTGCTGGCAAA
TGGCATGATCTTGGGGCTCATCTGTCTGGATCCAGACTGCGCACCCCCATGTACTTCTTCC
TGTCACACTTGGCCGTCATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGCTGGA
AAACCTAGTGAAACACAAAAAACTATCTCGTTCATCTCTTGCAATTATGCAGATGGCTTTG
TATTTGACTTTTGCTGCTGCAGTGTGCATGATTTTGGTGGTGATGTCCTATGACAGATTTGT
45 GGCGATCTGCCATCCCCTGCATTACACTGTCATCATGAAGTGGAGAGTGTGCACAGTACTG
GCTATTACTTCTGGGCATGTGGATTTTCCCTGGCCCTCATAAATCTAATTCTCCTTCTAAG
GCTGCCCTTCTGTGGGCCCCAGGAGGTGAACCACTTCTCGGTGAAATTCTGTCTGTCTCCTC
AACTGGCCTGTGCAGACACCTGGATTAATGAAATTTTTGTCTTTGCTGGTGGTGTGTTTG
TCTTAGTCGGGCCCCCTTTCTTGATGCTGATCTCCTACATGCGCATCCTCTTGGCCATCCTG
50 AAGATCCAGTCAAAGGAGGGCCGCAAAAAAGCCTTTCCACCTGCTCCTCCACCTCTGTG
TGTTTGGGCTTTACTTTGGCATGGCCATGGTGGTTTACCTGGTCCCAGACAACAGTCAACG
ACAGAAGCAGCAGAAAATTCTCACCCCTGTTTTACAGCCTTTTCAACCCATTGCTGAACCCC
CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCCTTATACAGAGCACTGCAGAAA
AAGAGGACCATGTGA (SEQ ID NO: 486).

55

AOLFR24B sequences:

MPSINDTHFYPPFFLLLGIPGLDTLHIWISFPFCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM
LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQMFFIHMFTGMETVLLVVMAYDRFVAICNP
LQYTMILTNTKISILASVVVGRNLVLVTPFVFLILRLPFCGHNIVPHTYCEHRGLAGLACAPIKIN
IYGLMVISYIIVDVILIASYVILIRAVFRLPSQDVRLKAFNTCGSHVCVMLCFYTPAFFSFMTH
RFGQNIPHYIHILLANLYVVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCTTCTATCAATGACACCCACTTCTATCCCCCTTCTTCCTCCTGCTAGGAATACCAGG
ACTGGACACTTTACATATCTGGATTCTTTCCCATTTCTGTATTGTGTACCTGATTGCCATTG
TGGGGAATATGACCATTCTCTTTGTGATCAAACTGAACATAGTCTACACCAGCCCATGTT
CTACTTCTGGCCATGTTGTCTATGATTGATCTGGGTCTGTCCACATCCACTATCCCCAAAA
TGCTAGGAATCTTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT
GTTCTTTATTCACATGTTTACAGGCATGGAGACTGTTCTGTTGGTGGTCATGGCTTATGACC
GCTTTGTTGCCATCTGCAACCCTCTCCAGTACACCATGATCCTCACCAATAAAACCATCAG
TATCCTAGCTTCTGTGGTTGTGGAAGAAATTTAGTTCTTGTAACCCCATTTGTGTTTCTCA
TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG
TCTGGCCGGGTTGGCCTGTGCACCCATTAAGATCAACATAATCTATGGGCTCATGGTGATT
TCTTATATTATTGTGGATGTGATCTTAATTGCCTCTTCTATGTGCTTATCCTTAGAGCTGT
TTTTCGCCTTCCCTCAAGATGTCCGACTAAAGGCCCTCAATACCTGTGGTTCTCATGTCT
GTGTTATGCTGTGCTTTTACACACCAGCATTTTTTTCTTTTATGACACATCGTTTTTGCCAA
AACATTCCCCACTATATCCATATTCTTTTGGCTAACCTGTATGTGGTTGTCCACCTGCCCT
TAACCTGTCAATTTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATATTT
GTACAGAAAGAATAA (SEQ ID NO: 488)

AOLFR33B sequences:

MLHTNNTQFHPSTFLVVGVPGLDVHVWIGFPFFAVYLTALLGNIILFVIQTEQSLHQPMFYFL
AMLAGTDLGLSTATIPKMLGIFWFNLGEIAGFCITQMYTIHICTGLESVVLTVTGIDRYAICNP
LRYSMILTNTKVIALGIVIVRTLTVFVTPFTFLTLRLPFCGVRIIPHTYCEHMLAKLACASINVIY
GLIAFSVGYIDISVIGFSYVQILRAVFHLPAPWDARLKALSTCGSHVCVMLAFYLPALFSFMTHRF
GHNIPHYIHILLANLYVVVPPALNSVIYGVKTKQIREQVLRILNPKSFWHFDPKRIFHNNSVRQ
(SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTCACCCTTCCACCTTCCTCGTAGTGCGGGGTCCCAG
GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCCTTCTTTGCGGTGTATCTAACAGCCCT
TCTAGGGAACATCATTATCCTGTTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG
TTTTACTTCTAGCCATGTTGGCCGGCACTGATCTGGGCTTGTCTACAGCAACCATCCCCA
AGATGCTGGGAATTTTCTGGTTTAATCTTGGAGAGATTGCATTTGGTGCCTGCATCACACA
GATGTATACCATTATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA
GATCGCTATATTGCCATCTGCAACCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA
TAGCCATTCTGGGCATAGTCATCATTGTCAGGACTTTGGTATTTGTGACTCCATTACATTT
CTCACCTGAGATTGCCTTTCTGTGGTGTCCGGATTATCCCTCATACCTATTGTGAACACAT
GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGATTGATTGCCTTCTCA
GTGGGATACATTGACATTTCTGTGATTGGATTTTCTATGTCCAGATCCTCCGAGCTGTCTT
CCATCTCCCAGCCTGGGATGCCCCGCTTAAGGCACTCAGCACATGTGGCTCTCACGTCTGT
GTTATGTTGGCTTTCTACCTGCCAGCCCTCTTTCTTCTCATGACACACCGCTTTGGCCACAA
CATCCCTCATTACATCCACATTCTTCTGGCCAATCTGTATGTGGTTTTTCCCCTGCTCTTA
ACTCTGTTATCTATGGGGTCAAAACAAAACAGATACGAGAGCAGGTACTTAGGATACTCA
ACCCTAAAAGCTTTTGGCATTTTGACCCCAAGAGGATCTTCCACAACAATTCAGTTAGACA
ATAA (SEQ ID NO: 490)

AOLFR112B sequences:

MKNKTVLTEFILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILILTLLDSHLQTPMYFFLRNFSF
LEISFTNIFPRVLISITTNKNSISFAGCFTQYFFAMFLGATEFYLLAAMSVDYVAICKPLHYTTI
MSSRICQLIFCSWLGGMLAIPTITLMSQQDFCASNRLNHYFCDYEPLELSCSDTSLIEKVFL
VASVTLVVTLLVLVLSYAFIKTILKLSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKEG
DTFNKGVALLITSVAPLLNPFYITLRNQVQKQPKDMVKLLNL (SEQ ID NO: 491)

ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCCTGAAC
TCCAGGTGGCAGTTTTTCACCTTTCTTTTCTTGGCGTATTTACTCAGCATCCTTGGAAATCTG
ACTATCCTCATCCTCACCTTGCTGGACTCCCACCTTCAGACTCCCATGTATTTCTTTCTCCG
5 GAACTTCTCCTTCTTGGAAATTTCCCTTCACAAACATCTTCATTCCAAGGGTCCGTGATTAGCA
TCACAACAGGGAACAAGAGTATCAGCTTTGCTGGCTGCTTCACTCAGTATTTCTTTGCCAT
GTTCTTGGGGCTACAGAGTTTTACCTTCTGGCTGCCATGTCCTATGACCGCTATGTGGCC
ATCTGCAAACCTCTGCATTACACCACCATCATGAGCAGCAGAATCTGCATCCAGCTGATTT
10 TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCTGATGAGTCAGCA
GGACTTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA
CTCTCATGTTTACAGACACAAGCCTCATAGAGAAGGTTGTCTTTCTTGTGGCATCTGTGACCC
TGGTGGTCACTCTGGTGCTAGTGATTCTCTCCTATGCATTATTATCAAGACTATTCTGAAG
CTCCCTCTGCCCAACAAGGACAAAAGCCTTTTCCACATGTTCTTCCCACATGATTGTGAT
15 CTCCCTCTCTTACGGAAGCTGCATGTTTATGTACATTAATCCCTCTGCAAAAAGAAGGGGAT
ACATTCAACAAGGGAGTAGCTCTACTCATTACTTCAGTTGCTCCTTTGTTGAACCCCTTTAT
TTACACCCTAAGGAACCAACAGGTAAAACAACCCTTCAAGGATATGGTCAAAAAGCTTCT
GAATCTTTAA (SEQ ID NO: 492)

AOLFR130B sequences:

20 MEGKNQTAPSEFIILGFDHLNELQYLLFTIFFLTYICTLGGNVFIIVVTIADSHLHTPMYYFLGNL
ALIDICYTTTNVPQMMVHLLSEKKIISYGGCVTQLFAFIFFVGSECLLLAAMAYDRYIAICKPLR
YSFIMNKALCSWLAASCSWTGFLNSVLHTVLTFFHLPCGNNQINYYFFCDIPLLILSCGDTSLNE
LALLSIGILISWTPFLCIILSYLYIISTILRISSEGRHKAFSTCASHLLIVILYYGSAIFTYVRPISSYS
LEKDRILISVLYSVVPMLNPVIYTLRNKDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)

25 ATGGAAGGAAAGAATCAAACAGCTCCATCTGAATTCATCATCTTGGGGTTCGACCACCTGA
ATGAATTGCAGTATTTACTCTTACCACCTCTTCTTTCTGACCTACATATGCACCTTAGGAGGC
AATGTTTTTATCATTGTGGTGACCATAGCTGATTCACCTACACACACCCATGTATTATTT
30 CCTAGGAAATCTTGCCCTTATTGACATCTGCTACACTACTACTAATGTCCCCCAGATGATG
GTGCATCTTCTGTGAGAGAAGAAAATCATTTCCTATGGAGGCTGTGTGACCCAGCTCTTTG
CATTCATTTTCTTTGTTGGCTCAGAGTGTCTCCTCCTGGCAGCAATGGCATATGATCGATAT
ATTGCTATCTGTAAGCCGTTAAGGTACTCATTATTATGAACAAGGCCCTGTGCAGCTGGT
TAGCAGCCTCATGCTGGACATGTGGGTTTCTCAACTCAGTGTGACACCGTTCTGACCTT
CCACCTGCCCTTCTGTGGTAACAATCAGATCAATTATTTCTTCTGTGACATACCTCCCTTGC
35 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAAGTGGCTTTGCTGTCCATTGGGATCCTC
ATAAGCTGGACTCCTTTCTGTGCATCATCTTTCTACCTTTACATCATCTCCACCATCCT
GAGGATCCGTTCTCTGAGGGGAGGCACAAAGCCTTTTCCACCTGTGCCTCCCACCTGCTC
ATTGTTATTCTCTATTATGGCAGTGCTATCTTACGTATGTGAGGCCCATCTCATCTTACTC
TCTAGAGAAAGATAGATTGATCTCAGTGCTGTATAGTGTGTGACACCCATGTCTGAATCCT
40 GTAATTTATACGTAAGGAATAAGGACATGAAGAGGCTGTGAAGGCCATAGGGAGAAAG
TGCAGCCACCAGTTTTCTTCTGATATATAA (SEQ ID NO: 494)

AOLFR142B sequences:

45 MARKDMAHINCTQATEFILVGLTDHQLKMPLFVLFSLIYLFVVGNLGLILLIRADTSLNTPM
YFFLSNLAFCYSSVITPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLLASMAYDRY
VAICNPLLYMVVMTGPGICQLVAVPYSYSFLMALFHTILTFRLSYCHSNIVNHFYCDDMPLRL
TCSDFTRFKQLWIFACAGIMFISSLLIVFVSYMFILSAILRMHSAEGRQKAFSTCGSHMLAVTIFYG
TLIFMYLQPSSSHALDTDKMASVFYTVIIPMLNPLIYSLQNKEVKEALKKIIINKN (SEQ ID NO:
495)

50 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATTCTTGTGG
GCCTCACAGACCATCAGGAGTTGAAGATGCCCTCTTTGTGCTATTCTTATCCATCTACCTC
TTCACAGTGGTAGGCAACTTGGGTTTGATCCTACTCATTAGAGCGGATACAAGTCTCAACA
CACCATTGTACTTCTTTCTTAGCAACCTAGCTTTTGTGGATTCTGTTACTCTTCTGTGATT
55 ACACCCAAAATGCTTGGGAATTTCTTGTACAAACAAAATGTTATATCCTTTGATGCATGTG
CTACTCAACTGGGCTGCTTTCTCACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG

GCCTATGACCGATATGTGGCCATTTGTAACCCTCTATTGTATATGGTTGTAATGACTCCAG
 GAATCTGCATTCAACTTGTAGCAGTTCCTTATAGCTATAGCTTCCTAATGGCACTATTTTAC
 ACCATCCTCACCTTCCGCCTCTCTATTGCCACTCCAACATTGTCAACCATTTCTATTGTGA
 5 TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT
 GCCTGTGCTGGTATCATGTTCAATTCCTCCCTTCTGATTGTCTTTGTCTCCTACATGTTCATC
 ATTTCTGCCATCCTGAGGATGCATTAGCTGAGGGAAGACAGAAGGCTTTCTCGACGTGTG
 GCTCTCACATGCTGGCAGTCACCATATTCTATGGGACCCTCATTTTTATGTACTTACAGCCT
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGTCTTCTACACAGTGATCATTC
 10 CCATGTTGAATCCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA
 AAATCATTATCAATAAAAACTAG (SEQ ID NO: 496)

AOLFR171C sequences:

MAEVNIIYVTVFILKGITNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL
 AFVDLCYSSAITPKMMVNFVVERNIPFHACATQLGCFLTFMITECFLLASMAFYDCYVAICSPL
 15 HYSTLMSRRVCIQLVAVPYIYSFLVALFHTVITFRLTYCGPNLINHFYCDDLPLALSCSDTHMK
 EILIFAFAGFDMISSSIVLTSYIFIIAILRIRSTQGQHKAISTCGSHMVTVTIFYGTLIFMYLQPKS
 NHSLDTDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQILFLKIRKLY (SEQ
 ID NO: 497)

20 ATGGCTGAAGTTAATATCATTTATGTCACTGTATTCACTCTGAAAGGAATTACCAACCGGC
 CAGAGCTTCAGGCCCCGTGCTTTGGGGTGTTTTAGTTATCTATCTGGTCACAGTGCTGGG
 CAATCTTGGGTTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTACTATT
 TCCTCAGCCACCTGGCCTTTGTTGACCTTTGTTACTCCTCTGCTATTACACCGAAGATGATG
 GTGAATTTTGTGTGGAACGCAACACCATTCCTTTCCATGCTTGTGCAACCCAACTGGGTT
 25 GTTTTCTCACCTTCATGATCACTAGTGTTCCTTCTAGCCTCCATGGCCTACGATTGCTAT
 GTCGCCATCTGTAGTCCCCTGCATTATTCAACACTGATGTCAAGAAGAGTCTGCATTCAAC
 TGGTGGCAGTTCATATATATACAGCTTCCTGGTTGCCCTCTTCCACACCGTTATCACTTTC
 CGTCTGACTTACTGTGGCCCAAACCTTAATTAACCATTTCTATTGTGATGACCTCCCCCTTCTT
 AGCTCTGTCCTGCTCAGACACACACATGAAGGAAATTCTGATATTTGCCCTTGTGCTGCTTT
 30 GATATGATCTCTTCTCTCCATTGTCTCACCTCCTACATCTTTATTATTGCCGCTATCCTA
 AGGATCCGCTCTACTCAGGGGCAACACAAAGCCATTTCACCTGTGGCTCCCATATGGTGA
 CTGTCACTATTTTCTATGGCACACTGATCTTTATGTACCTACAGCCCAAATCAAATCACTCC
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGATCCCCATGTTAAACCCCC
 35 TAATCTATAGTCTAAGGAACAAAGAAGTGAAAGATGCCTCAAAGAAAGCCTTGGATAAAG
 GTTGTGAAAACCTACAGATATTAACATTTTAAAAATAAGAAAACCTTTATTAA (SEQ ID NO:
 498)

AOLFR225B sequences:

MKNRTMFGEFILLGLTNQPELQVMIFIFLFLTYMLSILGNLTIITLTLDDPHLQTPMYFFLRNFSF
 40 LEISFTSIFIPRFLTSMTTGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAICKPLHYLTI
 MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFCVSNILNHYYCDYGPLVELACSDTSLLELMVI
 LLAVVTLMTLVLVLTLSYTYIIRTILRIPSAQQRTKAFSTCSSHMIVISLSYGSCMFMYNPSAKE
 GGA FNKGIAVLITSVTPLLPFIYTLRNQQVKQAFKDSVKKIVKL (SEQ ID NO: 499)

45 ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCTTACAAATCAACCTGAAC
 TCCAAGTGATGATATTCATCTTTCTGTTCCTCACCTACATGCTAAGTATCCTAGGAAATCTG
 ACTATTATCACCTCACCTTACTAGACCCCCACCTCCAGACCCCCATGTATTTCTTCTCCG
 GAATTTCTCCTTCTTAGAAATTTCTTACATCCATTTTTATTCCAGATTTCTGACCAGCA
 TGACAAACAGGAAATAAAGTTATCAGCTTTGCTGGCTGCTTGACTCAGTATTTTTTGTCTAT
 50 ATTTCTGGAGCTACCGAGTTTACCTCCTGGCCTCCATGTCTTATGATCGTTATGTGGCCA
 TCTGCAAAACCCTTGCAATTACCTAGCACTATTATGAGCAGCAGAGTCTGCATACAACCTAGTGT
 CTGCTCCTGGTTGGGGGGATTCTAGCAATCTTACCACCAATCATCCTGATGACCCAGGTA
 GATTTCTGTGTCTCCAACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGGAGCT
 TGCCTGCTCAGACACAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTC
 55 ATGGTTACTCTGGTGCTGGTGACACTTTCTTACACATACATTATCAGGACTATTCTGAGGA
 TCCCTTCTGCCAGCAAAGGACAAAGGCCTTTTCCACTTGTTCTCCCATGATTGTCATC

NELVLFTVFGFIELSTISGVFISYCYIILSVLEIHS A EGRFKALSTCTSHLSAVAIFQGTLLFMYFRP
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKEALKKLKNKILF (SEQ ID NO: 505)

5 ATGGACTGGGAAAATTGCTCCTCATTAAGTATTTTTTCTCTTGGGAATTACCAATAACCC
AGAGATGAAAGTGACCCTATTTGCTGTATTCTTGGCTGTTTATATCATTAATTTCTCAGCAA
ATCTTGGAATGATAGTTTTAATCAGAATGGATTACCAACTTCACACACCAATGTATTTCTT
CCTCAGTCATCTGTCTTTCTGTGATCTCTGCTATTCTACTGCAACTGGGCCCAAGATGCTGG
TAGATCTACTTGCCAAGAACAAGTCAATACCCTTCTATGGCTGTGCTCTGCAATTCTTGGT
CTTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTGCTGATGGCCTTTGATCGGTACA
10 AGGCCATCATCAACCCCTGCTCTATACAGTCAACATGTCTAGCAGAGTGTGCTATCTACT
CTTGACTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC
CGCCTATGCTTCTGTGGGTCTAATGAGATTAATCATTTCTTCTGTGATATCCCTCCTCTCTT
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTATTACCGTCTTTGGTTTTA
TTGAACTGAGTACCATTTCAGGAGTTTTCAATTTCTTATTGTTATATCATCCTATCAGTCTTG
15 GAGATACACTCTGCTGAGGGGAGGTTCAAAGCTCTCTACATGCACTTCCCATTATCTG
CGGTTGCAATTTTCCAGGGAACCTGCTCTTTATGTATTTCCGGCCAAGTTCTTCTTCTTCT
CTAGATCAAGATAAAAATGACCTCATTGTTTTACACCTTGTGGTTCCTATGTTGAACCCCT
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAACTGAAAAATAAAAT
TTTATTTTAA (SEQ ID NO: 506)

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AOLFR314 sequences:

MEVKNCCMVTEFILLGIPHTEGLEMTLFLVFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG
NLSVFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFHFLGSI ECF LFTVMAYDRFTAICY
PLRYTVIMNPRICVALAVGTWLLGCIHSSILTS LFTLPYCGPNEVDHFFCDIPALLPLACADTSL
25 AQRVSFTNVGLISLVCFLLILLSYTRITISILSIRTT EGRRRAFSTCSAHLIAILCAYGPIITVYLQPT
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVK TALKTILHRTGHVPES (SEQ ID NO: 507)

30 ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTCATCCTTTTGGGAATCCCACACACA
GAGGGGCTGGAGATGACACTTTTTGTCTTATTTCTTGCCCTTCTATGCCTGCACTCTACTGGG
AAATGTGTCTATCCTTGTGTGTTATGTCTTCTGCTCGCCTTCACACACCTATGTATTTCT
TCCTGGGAAACTTGTCTGTGTTTGACATGGGTTTCTCCTCAGTGACTTGTCCCAAAATGCT
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT
TCTTCCATTTCTCGGGAGCATTGAGTGCTTCTTGTTTACGGTGATGGCCTATGACCGCTTC
ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC
35 TGGCTGTGGGCACATGGCTGTTAGGGTGCAATTCATTCCAGTATCTTGACCTCCCTCACCTTC
ACCTTGCCATACTGTGGTCCCAATGAAGTGGATCACTTCTTCTGTGACATTCCAGCACTGTT
GCCCTTGGCCTGTGCTGACACATCCTTAGCCAGAGGGTGAGCTTACCAACGTTGGCCTC
ATATCTCTTGTCTGCTTTCTGCTAATTCTTTTATCCTACACTAGAATCACAATATCTATCTT
AAGCATTCGTACAACCTGAGGGCCGTCGCCGTGCCTTCTCCACCTGCAGTGCTCACCTCATT
40 GCCATCCTCTGTGCTATGGGCCCATCATCACTGTCTACCTGCAGCCCACACCCAACCCCA
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCTTTGAT
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAACAATATTGCACAGGACAGG
CCATGTTCCCTGAGAGTTAG (SEQ ID NO: 508)

45

AOLFR324B sequences:

MPIANDTQFHTSSFLLLIPGLEDVHIWIGFPFFSVYLIALLGNAAIFFVITQEQSLHEPMTYYCLA
MLDSIDLSTATIPKMLGIFWFNIKEISFGGYLSQMFFIHFFTVMESIVLVAMAFDRYIAICKPL
WYTMILTSKIISLIAGIAVLRLSYMVIPLVFLLLRPLFCGHRIPHTYCEHMGRIARLACASIKVNIM
FGLGSISLLLLDVLLIILSHIRILYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH
50 DIPQYIHIFLANLYVVVPPTLNPVIYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCCATACTTCTTCATTCTCTACTGCTGGGTATCCCAGG
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTTTTCTCTGTGTATCTTATTGCACTCC
TGGGAAATGCTGCTATCTTCTTTGTGATCCAACTGAGCAGAGTCTCCATGAGCCCATGTA
55 CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTTGTCTACGGCCACCATTTCCAAA
ATGCTGGGCATCTTCTGGTTCAATATCAAGGAAATATCTTTTGGAGGCTACCTTTCTCAGA

5 TGTCTTCATCCATTTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC
 CGCTACATTGCCATTTGCAAACCTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA
 GCCTCATTGCAGGCATTGCTGTCCTGAGGAGCTTGTACATGGTCATTCCACTGGTGTCTCT
 CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG
 10 GCATTGCCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT
 TTCTCTCTTGTTATTGGATGTGCTCCTTATTATTCTCTCCCATATCAGGATCCTCTATGCTGT
 CTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT
 GGTGTTATCTTAGCCTTTTCTACACCAGCATTTTTCTCTTTCTTTACACACTGCTTTGGCCAT
 GATATTCCCCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTTGTTCTCTCCACCCT
 15 CAATCCTGTAATCTATGGGGTCAGAACCAACATATTAGGGAGACAGTGCTGAGGATTTTC
 TTCAAGACAGATCACTAA (SEQ ID NO: 510)

AOLFR328 sequences:

15 MALGNHSTITEFLLLGLSADPNIRALLFVFLGIYLLTIMENLMLLLVIRADSCLHKPMYFFLSH
 LSFVDLCFSSVIVPKMLENLLSQRKTISVEGCLAQVFFVFTAGTEACLLSGMAYDRHAAIRRP
 LLYGQIMGKQLYMHLVWGSWGLGFLDALINVLLAVNMVFCFAKIIHHYSYEMPSLLPLSCSDI
 SRSLIVLLCSTLLHGLGNFLLVFLSYTRIISTILSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL
 MPNSGSPIELIFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGCACCATCACCGAGTTCCTCCTCCTTGGGCTGTCTGCCGACC
 CCAACATCCGGGCTCTGCTCTTTGTGCTGTTCTGGGGATTACCTCCTGACCATAATGGA
 AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGTCTCCATAAGCCCATGTATTTCT
 TCCTGAGTCACCTCTCTTTTGTGATCTCTGCTTCTCTTCAGTCATTGTGCCCAAGATGCTG
 25 GAGAACCTCCTGTACAGAGGAAAACCATTTTCAGTAGAGGGCTGCCTGGCTCAGGTCTTCT
 TTGTGTTTGTCACTGCAGGGACTGAAGCCTGCCTTCTCTCAGGGATGGCCTATGACCGCCA
 TGCTGCCATCCGCCGCCCACTACTTTATGGACAGATCATGGGTAAACAGCTGTATATGCAC
 CTTGTGTGGGGCTCATGGGGACTGGGCTTTCTGGACGCACTCATCAATGTCTCCTAGCTG
 TAAACATGGTCTTTTGTGAAGCCAAAATCATTACCACTACAGCTATGAGATGCCATCCCT
 CCTCCCTCTGTCTGCTCTGATATCTCCAGAAGCCTCATCGTTTTGCTCTGCTCCACTCTCC
 30 TACATGGGCTGGGAAACTTCCTTTTGGTCTTCTTATCCTACACCCGTATAATCTCTACCATC
 CTAAGCATCAGCTCTACCTCGGGCAGAAGCAAGGCCTTCTCCACCTGCTCTGCCACCTCA
 CTGCAGTGACACTTTACTATGGCTCAGGTTTGTCTCCGCCATCTCATGCCAAACTCAGGTTT
 CCCCATAGAGTTGATCTTCTCTGTGCAGTATACTGTAGTCACTCCCATGCTGAATTCCTCA
 TCTATAGCCTGAAAAATAAGGAAGTGAAGGTAGCTCTGAAAAGAACTTTGGAAAAATATT
 35 TGCAATATACCAGACGTTGA (SEQ ID NO: 512)